

C: Superfamily: immunoglobulin C region; immunoglobulin homology
 C: Keywords: T-cell receptor
 F: 24-98/Domain: immunoglobulin homology <IMM>

C:Genetics:
 A:Gene: v-Tar
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimeric
 F: 24-98/Domain: immunoglobulin homology <IMM>
 F: 151-172/Domain: transmembrane #status predicted <TMM>
 F: 173-177/Domain: intracellular #status predicted <INT>
 F: 31-56/disulfide bonds: #status predicted

Query Match 9 Score 763.5; DB 2; Length 178;
 Best Local Similarity 80.3%; Pred. No. 6, 2e-53;
 Matches 143; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

QY 136 EDLKNVFPPEVAVEPSEAEISHTQRATLVCLATGFPDPHVLSWVNGKEVHSGYSTDP 195
 DB 1 DDLQVRPDKVAVFEPSEAEISRTQRATLVCLATGFPDPHVLSWVNGKQYQGVSTD 60

QY 196 QPKEQPAINDSYCLSSRLRVTSATEQNPRHFCRQYQFLSENDEWTQDRAKPVTOI 255
 DB 61 QPYKEEDPSRNDSSCYCLSSRLRVTSATEQNPRHFCRQYQFLTDEWEYNWTKPTQN 120

QY 256 VSAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 312
 DB 121 ISAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMATVKKDS 177

RESULT 9
 P00076 T-cell receptor beta chain (BTB13 c beta 2) - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 A:Accession: PQ0076
 R: Tanaka, A.; Ishiguro, N.; Shinagawa, M.
 A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
 Submitted to JIPID, May 1990
 A:Reference number: J00472
 A:Accession: FQ0076
 A: Molecule type: mRNA
 A:Residues: 1-178 <TAN>
 A:Experimental source: T cell
 C:Genetics:
 A:Gene: BTB13 c beta 2
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: receptor
 F: 24-98/Domain: immunoglobulin homology <IMM>

Query Match 45.9%; Score 763.5; DB 2; Length 178;
 Best Local Similarity 80.3%; Pred. No. 2e-52;
 Matches 143; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

QY 136 EDLKNVFPPEVAVEPSEAEISHTQRATLVCLATGFPDPHVLSWVNGKEVHSGYSTDP 195
 DB 1 DDLQVRPDKVAVFEPSEAEISRTQRATLVCLATGFPDPHVLSWVNGKQYQGVSTD 60

QY 196 QPKEQPAINDSYCLSSRLRVTSATEQNPRHFCRQYQFLSENDEWTQDRAKPVTOI 254
 DB 61 EPIKEDPARDSYCLSSRLRVTSATEQNPRHFCRQYQFLTDODQWEQNRTKPTQ 120

QY 256 VSAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 312
 DB 121 NSAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 178

RESULT 10
 RWATC T-cell receptor beta chain C region homolog (T17T-22) - feline leukemia virus

C:Species: feline leukemia virus
 C:Accession: 31-Mar-1989 #sequence_revision 30-Sep-1993 #text_change 23-Aug-1997
 R:Fulton, R.; Forrest, D.; McFarlane, R.; Onions, D.; Neil, J. C.

Nature 326, 190-194, 1987
 A:Reference number: A26600; MUTD:87144638
 A:Accession: C26600
 A:Molecule type: DNA
 A:Residues: 1-177 <FUL>

C:Genetics:
 A:Gene: v-Tar
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimeric
 F: 24-98/Domain: immunoglobulin homology <IMM>

C:Genetics:
 A:Gene: v-Tar
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimeric
 F: 24-98/Domain: immunoglobulin homology <IMM>

Query Match 45.1%; Score 750; DB 1; Length 177;
 Best Local Similarity 80.2%; Pred. No. 2e-51;
 Matches 142; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 136 EDLKNVFPPEVAVEPSEAEISHTQRATLVCLATGFPDPHVLSWVNGKEVHSGYSTDP 195
 DB 1 EDLKVSPKVTVLOPSEAEISRLKATLVCLATGFPDVHLSWVNGKEVHSGYSTDP 60

QY 196 QPKEQPAINDSYCLSSRLRVTSATEQNPRHFCRQYQFLSENDEWTQDRAKPVTOI 255
 DB 61 EPYKEOSGANSSYCLSSRLRVTSATEWNHPRHFCRQYQFLDQHGLQDDNDYPRAKPVTOI 120

QY 256 VSAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 312
 DB 121 VSADWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 177

RESULT 11
 T-cell receptor beta-1 chain C region - shrew mouse

C:Species: Mus pahari

C:Accession: A46547 #sequence_revision 17-Feb-1994 #text_change 21-Jan-2000
 R:Jouvin-Marche, E.; Heller, M.; Rudikoff, S.
 J. Exp. Med. 161, 2083-2088, 1986

A:Title: Gene correction in the evolution of the T cell receptor beta chain.
 A:Reference number: A46547; MUID:87059557
 A:Accession: A46547
 A:Cross-references: GB: M28600
 C:Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 A: Molecule type: DNA
 A: Residues: 1-173 <OOU>
 A:Status: preliminary
 A:Accession: A46547
 A:Cross-references: GB: M28600
 C:Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>

Query Match 44.5%; Score 741; DB 2; Length 173;
 Best Local Similarity 79.7%; Pred. No. 1.e-50;
 Matches 141; Conservative 13; Mismatches 19; Indels 4; Gaps 1;

QY 136 EDLKNVFPPEVAVEPSEAEISHTQRATLVCLATGFPDPHVLSWVNGKEVHSGYSTDP 195
 DB 1 EDLKVTPKVSLPEPSEAEISRLKATLVCLATGFPDVHLSWVNGKEVHSGYSTDP 195

QY 196 QPKEQPAINDSYCLSSRLRVTSATEQNPRHFCRQYQFLSENDEWTQDRAKPVTOI 254
 DB 1 EDLKVTPKVSLPEPSEAEISRLKATLVCLATGFPDVHLSWVNGKEVHSGYSTDP 60

QY 196 QPKEQPAINDSYCLSSRLRVTSATEQNPRHFCRQYQFLSENDEWTQDRAKPVTOI 255
 DB 61 QAYKE---SNNSYCLSSRLRVTSATEWNHPRHFCRQYQFLDQHGLQDDNDYPRAKPVTOI 116

QY 256 VSAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 312
 DB 117 ISAEAWGRADCGETSESYQGVLSATTLYEILLGKATLYAVLYSALVLMAMVKRKS 173

RESULT 12
 RWBB T-cell receptor beta chain precursor (ANA 11) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Accession: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
 R:Angiolillo, A.L.; Lamoyi, E.; Bernstein, K.E.; Mage, R.G.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4498-4502, 1985

A:Title: Identification of genes for the constant region of rabbit T-cell receptor be

A; Reference number: A94052; MUID:85242712
 A; Accession: A94052
 A; Molecule type: mRNA
 A; Residues: 1-319 <ANG>
 R; Mage, R.
 submitted to the Protein Sequence Database, April 1987
 A; Reference number: A9616
 A; Content: Corrections to residues 79-83 and 104-105
 A; Accession: A94616
 A; Molecule type: mRNA
 A; Residues: 79-83,104-105 <MAG>
 C; Superfamily: immunoglobulin C region; immunoglobulin homology
 C; Keywords: glycoprotein; heterotrimer; T-cell receptor; transmembrane protein
 F; 166-240/Domain: immunoglobulin homology <IMM>
 P; 292-313/Domain: transmembrane #status predicted <INT>
 F; 314-318/Domain: intracellular #status predicted <INT>
 F; 147,164,254,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.2%; Score 736; DB 1; Length 173;
 Best Local Similarity 79.1%; Pred. No. 2.6e-50;
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 136 EDLKNYFPEVAFPESEAELSHTOKATLYCLATGFYDPDVELSKWVNGKEVHSGVSTDP 195
 Db 1 EDLKNYFPEVAFPESEAELSHTOKATLYCLATGFYDPDVELSKWVNGKEVHSGVSTDP 60

Qy 196 QPLKEQPALNDSCRYCLSRLRVSATFWQNPNHFRCQVQFYGLSENDEWTQDRAKPTQI 255
 Db 61 QAYKE---SNYSYCSRLRVSATFWNPNHFRCQVQFHGLSDEKDKEPEGSPPPTQN 116

Qy 256 VSAEANGRADCGFTSEYQQGVLSATILYEILIGRATLYAVLVSALVLMAMVKRKDS 312
 Db 117 ISAEANGRADCGITSAQQGVLSATILYEILIGRATLYAVLVSALVLMAMVKRKNS 173

RESULT 14

Qy 190 GYSTDPQPLIKEQPALNDSCRYCLSRLRVSATFWQNPNHFRCQVQFYGLSENDEWTQDRA 249
 Db 197 GYSTDPQYKQDPSPSDHEKYCLSSRLRVSAWTHPNPNHFRCQVQFYGLDDENTYNS 256

Qy 250 KPYQTIVSAEAWGRADCSEFTSESYQQGVLSATILYEILIGRATLYAVLVSALVLMAMVKR 309
 Db 257 KPTQNTIAHTRGADCGTSASYYVDFPSEAENKTQATLYCLAKDTPDVELSKWVNGKEVHN 316

Qy 310 KDS 312
 Db 317 KDS 319

RESULT 13

PWMS1C
 T-cell receptor beta-1 chain C region - mouse
 C; Species: Mus musculus (house mouse)
 ; Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 16-Aug-1996
 R; Gascogne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalali, J.; Davis, M.M.
 Nature 310, 387-391, 1984
 A; Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and variable domains
 A; Reference number: A93336; MUID:8427074
 A; Accession: B93336
 A; Molecule type: DNA
 A; Residues: 1-173 <GAS>
 A; Cross references: GB:M26053
 A; Experimental source: strain B10.A, cytotoxic T lymphocyte
 R; Hedrick, S.M.; Nielsen, E.A.; Kavalali, J.; Cohen, D.I.; Davis, M.M.
 Nature 308, 153-158, 1984
 A; Title: Sequence relationships between T-cell receptor polypeptides and immunoglobulins
 A; Reference number: A93325
 A; Molecule type: mRNA
 A; Residues: 1-69, H, 71-173 <HED>
 A; Cross references: GB:K01080
 A; Experimental source: clone 86T1
 A; Note: the authors translated the codon TAT for residue 134 as Val
 R; Morinaga, T.; Foredar, A.; Singh, B.; Wiesmann, T.G.; Tamaki, T.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8163-8167, 1985
 A; Title: Isolation of cDNA clones encoding a T-cell receptor beta-chain from a beef insulinoma cell line
 A; Reference number: A94078; MUID:8606806
 A; Accession: A23572
 A; Molecule type: mRNA
 A; Residues: 1-173 <MCR>
 A; Cross references: GB:M11456
 C; Species: Mus musculus (house mouse) - mouse

RESULT 15

RWSBC
 T-cell receptor beta-2 chain C region - mouse

C; Date: 03-Aug-1984 #sequence-revision 28-Feb-1986 #text-change 05-Sep-1997
 C; Accession: A93336; B93333; A02134
 R; Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalali, J.; Davis, M.M.
 A; Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and j
 A; Reference number: A93336; MUID:84270704
 A; Accession: A93336
 A; Molecule type: DNA
 A; Residues: 1-173 <GA>
 A; Experimental source: strain B10.A, cytotoxic T lymphocyte
 R; Saito, H.; Kranz, D.M.; Takagaki, Y.; Hayday, A.C.; Eisen, H.N.; Tonegawa, S.
 Nature 309, 757-762, 1984
 A; Title: Complete primary structure of a heterodimeric T-cell receptor deduced from cDNA
 A; Reference number: A93333; MUID:84245824
 A; Accession: B93333
 A; Molecule type: mRNA
 A; Residues: 1-49, 'R', 51-69, 'H', 71-173 <SAI>
 A; Experimental source: BALB.B, clone 2C, cytotoxic T lymphocyte
 C; Genetics:
 A; Introns: 1/1; 126/1; 132/1; 163/3
 C; Superfamily: immunoglobulin C region; immunoglobulin homology
 C; Keywords: glycoprotein; heterotrimer; receptor; T-cell; transmembrane protein
 F; 24-94 /Domain: immunoglobulin homology <IMM>
 F; 147-168 /Domain: immunoglobulin homology <IMM>
 F; 169-173 /Domain: transmembrane #status predicted <NT>
 F; 67-116 /Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	Score	DB 1:	Length
Best Local Similarity	43.9%	Score 731;	173;
Matches	139;	Conservative	78.5%; Pred. No. 6.4e-50;
	16;	Mismatches	16;
	18;	Indels	4;
		Gaps	1;
Oy	136	EDLKNVFPPEVAYPEPSEAEISHTOKATUCLATGEPDPDHYLSWWNGKEWHSGYSTD	195
Db	1	EDLERNVTPEPKVSLFEPSPKAEIAKOKATLVCARGEPPDRHLSWWNGKEWHSGYSTD	60
Oy	196	QPLKEQPALNDSRYCLSSLRLRVSATFWONPRHFRCOVFTYGLSENEDTQDRAKPTQI	255
Db	61	QAYKE----SNSYCLSSLRLRVSATFWHNPRAHFRCOVQFHLSEDDKWPECSPKVTON	116
Oy	256	VSAFAWGRADCGFTSESYQGVLSATILYEILIGKATLYAVLVSALVLMAVKRKDS	312
Db	117	ISAFAWGRADCGITSASYHQGVLSATILYEILIGKATLYAVLVSGLVLMAMWKKNS	173

Search completed: October 11, 2000, 06:09:02
 Job time: 51 sec

Run on:	October 11, 2000, 06:08:11 ;	Search time 9.53 Seconds (without alignments)	
Title:	US-09-405-940-[]	1021.047 Million cell updates/sec	
COM protein - protein search, using sw model			
Gencore version 4.5			
Copyright (c) 1993 - 2000 Compugen Ltd.			
34	137.5	8.3	438
35	137	8.2	368
36	136.5	8.2	421
37	135.5	8.1	353
38	133.5	8.0	353
39	133	8.0	340
40	132.5	8.0	399
41	131.2	7.9	135
42	131.5	7.9	298
43	131.5	7.9	365
44	131.5	7.9	393
45	131	7.9	136
P23085	heterodontu		
P14477	mus musculu		
P06336	mus musculu		
P01876	homo sapien		
P20758	gorilla gor		
P01877	homo sapien		
P01865	mus musculu		
P01740	mus musculu		
P01895	mus musculu		
P01390	mus musculu		
P23086	heterodontu		
P03279	homo sapien		
HVC2_HETER			
HAL1_MOUSE			
EPC_MOUSE			
ALC1_HUMAN			
ALC1_GORGO			
ALC2_HUMAN			
GCAM_MOUSE			
TVCL_MOUSE			
HALY_MOUSE			
HAL2_MOUSE			
HVC3_HETFER			
HUMAN			

Scoring table: BLOSUM62
Sequence: MGRDQWAALLULGADHRS.....AVLVSAVLMLAMVKKRDSRG 314

Searched: 85661 seen 30989116 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results pre-

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

QY 121 YNEQ-YFGPGTRLTVLEDLKNVFPPEVAVFPESEAFISHTOKATLVCLATGFYPDHVELS 179
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 DB 129 YGETLYFGEGSRLTIVEDLKVSSPRKVTVEESEAFISRTLKATLVCLATGFYPDHVELS 188
 "Identification of genes for the constant region of rabbit T-cell receptor beta chains.";
 "Receptor beta chains."
 RT
 RL
 RN
 RP
 REVISIONS TO 79-83 AND 104-105.
 RA
 Mage R.G.;
 Submitted (APR-1987) to the PIR data bank.
 DR
 PIR: A02136; PWRRB.
 DR
 PFAM: PF00047; iqg_1.
 KW
 T-CELL; Receptor; Transmembrane; Glycoprotein.
 FT
 DOMAIN 142 273 C REGION.
 FT
 TRANSMEM 292 313 CYTOPLASMIC TAIL.
 FT
 DOMAIN 314 319 CYTOPLASMIC TAIL.
 FT
 CARBOHYD 147 147 POTENTIAL.
 FT
 CARBOHYD 164 164 POTENTIAL.
 FT
 CARBOHYD 254 254 POTENTIAL.
 FT
 CARBOHYD 262 262 POTENTIAL.
 SQ 319 AA: 36068 MW; Aad2C3035ED45306 CRC64;

RESULT 2

TCB_HUMAN	STANDARD;	PRT;	177 AA.
ID	TCHUMAN		
AC	PO1650;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DE	T-CELL RECEPTOR BETA CHAIN C REGION.		
OS	Homo sapiens (Human).		
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
FN	[1]		
RP	SEQUENCE FROM N.A. (CLONE YT35).		
RX	MEDLINE: 84142269.		
RA	Yanagi Y., Yoshikai Y., Leggett K., Clark S.P., Aleksander I., Mak T.W.;		
RT	"A human T cell-specific cDNA clone encodes a protein having extensive homology to immunoglobulin chains.", Nature 308:145-149(1984). RL PIR; A02133; RWIUCY.		
DR	PFAM: PF00047; iqg_1.		
KW	T-cell, Receptor.		
SQ	SEQUENCE 177 AA: 19898 MW; 9242AAAE3DB4AE CRC64;		

Query Match 54.5%; Score 907; DB 1; Length 177;
 Best Local Similarity 97.7%; Pred. No. 1.5e-69; Indels 0; Gaps 0;

Matches 1/2; Conservative 1; Mismatches 3; Standard; PRT; 173 AA.

RESULT 4

TCB1_MOUSE	STANDARD;	PRT;	173 AA.
ID	TCB1_MOUSE		
AC	PO152;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1996 (Rel. 01, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	T-CELL RECEPTOR BETA-1 CHAIN C REGION.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
STRAIN=B10.A;			
RX	MEDLINE: 84270074.		
RA	Gascogne N.R.J., Chien Y., Becker D.M., Kavalier J., Davis M.M.;		
RT	"Genomic organization and sequence of T-cell receptor beta-chain constant- and joining-region genes.";		
RL	Nature 310:387-391(1984).		

RN [2]

SEQUENCE FROM N.A. (CLONE 86T1).

RX MEDLINE: 84142271.

RX Heddick S.M., Nielsen E.A., Kavalier J., Cohen D.I., Davis M.M.;

RT "Sequence relationships between putative T-cell receptor polypeptides and immunoglobulins."

RT Nature 308:153-158(1984).

CC -!- MISCELLANEOUS: REF 2. AUTHORS TRANSLATED THE CODON TAT FOR RESIDUE CC 134 AS VAL.

CC -!- MISCELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T

RESULT 3

TCB1_RABBIT	STANDARD;	PRT;	319 AA.
ID	TCB1_RABBIT		
AC	PO633;		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	15-FEB-2000 (Rel. 39, Last annotation update)		
DE	T-CELL RECEPTOR BETA CHAIN A11.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
RN	[1]		

CC	-!- LYMPHOCYTE.	Query Match Score 43.9%; Best Local Similarity 73.1%; Pred. No. 9.4e-55; Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;
CC	-!- MICELLANEOUS: CLONE 86T1 WAS ISOLATED FROM A CYTOTOXIC T	
CC	LYMPHOCYTE.	
DR	PTR; A02135; RWS1C.	
PFAM	FT00047; 19; 1.	
KW	T-cell; Receptor; Transmembrane; Glycoprotein.	
FT	NON_TER 1 1 C REGION.	
FT	TRANSFM 1 146 POTENTIAL.	
FT	DOMAIN 146 167 CYTOPLASMIC TAIL.	
FT	DOMAIN 168 173 Y -> H (IN CLONE 86T1).	
FT	VARIANT 70 70 MW: F9B4735E46D3EAD7 CRC64;	
SQ	SEQUENCE 173 AA: 19346 ;	Score 44.2%; Best Local Similarity 79.1%; Pred. No. 3.6e-55; Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;
Query Match Score 43.9%; Best Local Similarity 73.1%; Pred. No. 9.4e-55; Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;	Query Match Score 43.9%; Best Local Similarity 78.5%; Pred. No. 9.4e-55; Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;	
Qy	EDLKVFPPEVAVEPSEAEISHTOKATVCLATGFYPPDHVELSWWNGKEVHSGVSTDP 195	Qy 136 EDLKVFPPEVAVEPSEAEISHTOKATVCLATGFYPPDHVELSWWNGKEVHSGVSTDP 195
Db	1 EDLNVTPKRVSEPSKATVCLATGFYPPDHVELSWWNGKEVHSGVSTDP 60	Db 1 EDLNVTPKRVSEPSKATVCLATGFYPPDHVELSWWNGKEVHSGVSTDP 60
Qy	QPLKEQPALNDSRVCLSSRVSATEWQNPNPNHERCQVQFYGLSENDEWTQDRAKPVTQI 255	Qy 196 QPLKEQPALNDSRVCLSSRVSATEWQNPNPNHERCQVQFYGLSENDEWTQDRAKPVTQI 255
Db	61 QAYKE--SNYSCLSSRVSATEWQNPNPNHERCQVQFYGLSENDEWTQDRAKPVTQI 116	Db 61 QAYKE--SNYSCLSSRVSATEWQNPNPNHERCQVQFYGLSENDEWTQDRAKPVTQI 255
Qy	256 VSAEAWGRADCFTSESYQQGVLSATLTYELLGKATLYAVLVSLVMAVMKRDS 312	Qy 256 VSAEAWGRADCFTSESYQQGVLSATLTYELLGKATLYAVLVSLVMAVMKRDS 312
Db	117 VSAEAWGRADCFTSASYQQGVLSATLTYELLGKATLYAVLVSLVMAVMKRDS 173	Db 117 VSAEAWGRADCFTSASYQQGVLSATLTYELLGKATLYAVLVSLVMAVMKRDS 173
RESULT 5	TC2_MOUSE STANDARD; PRT; 173 AA.	RESULT 6
AC	TCB2_MOUSE STANDARD; PRT; 173 AA.	TVB2_HUMAN STANDARD; PRT; 133 AA.
PO1851;		ID TVB2_HUMAN
DT	21-JUL-1986 (Rel. 01, Created)	AC P0445;
DT	21-JUL-1986 (Rel. 01, Last sequence update)	DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT	21-JUL-1986 (Rel. 01, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE	T-CELL RECEPTOR BETA-2 CHAIN C REGION.	DB T-CELL RECEPTOR BETA CHAIN V REGION CTL-L17 PRECURSOR.
OS	Mus musculus (Mouse).	GN TCRB.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OS Homo sapiens (Human).
OC		CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]	CC [1]
RP	SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RX	MEDLINE; 862/67/0.	RX MEDLINE; 862/67/0.
RA	Leiden J.M., Fraser J.D., Strominger J.L.;	RA "The complete primary structure of the T-cell receptor genes from an alloreactive cytotoxic human T-lymphocyte clone."
RT		RL Immunogenetics 24:17-23 (1986).
CC	-!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC T-LYMPHOCHITE THAT IS T3+, T4+, T8+.	CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC T-LYMPHOCHITE THAT IS T3+, T4+, T8+.
CC		-- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).
DR	M15564; AAA61027.1; -.	CC DR EMBL; M15564; AAA61027.1; -.
DR	PTR; A02001; RWHU7B.	CC DR PTR; A02001; RWHU7B.
DR	PFAM: PF00047; iq; 1.	CC DR PFAM: PF00047; iq; 1.
KW	T-cell; Receptor; Glycoprotein; Signal.	CC KW T-CELL RECEPTOR BETA CHAIN V REGION CTL-L17.
FT	SIGNAL 1 21	FT SIGNAL 1 21
FT	CHAIN 22 133	FT CHAIN 22 133
FT	DOMAIN 22 114	FT DOMAIN 22 114
FT	DOMAIN 115 118	FT DOMAIN 115 118
FT	CARBOHYD 30 30	FT CARBOHYD 30 30
FT	DISULFID 37 37	FT DISULFID 37 37
FT	NON_TER 42 111	FT NON_TER 42 111
SQ	SEQUENCE 133 AA; 14999 MW; 21030818D341F CRC64;	FT NON_TER 133 133
DR	SEQUENCE FROM N.A. (CLONE 2C).	SQ SEQUENCE 133 AA; 14999 MW; 21030818D341F CRC64;
RC	STRAIN-BALB-B;	
RX	MEDLINE; 84245824.	
RA	Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N., Tonegawa S.;	
RA	"Complete primary structure of a heterodimeric T-cell receptor deduced from cDNA sequences;"	
RT	Nature 309:757-762(1984).	
RT	-!- MICELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T	
CC	LYMPHOCYTE.	
CC	-!- MICELLANEOUS: CLONE 2C WAS ISOLATED FROM A CYTOTOXIC T	
CC	LYMPHOCYTE.	
PTR	A02134; RWS1C.	
PFAM	FT00047; 1.	
KW	T-cell; Receptor; Transmembrane; Glycoprotein.	
FT	NON_TER 1 1 C REGION.	
FT	DOMAIN 1 146	
FT	TRANSFM 147 168	
FT	DOMAIN 169 173 CYTOPLASMIC TAIL.	
FT	VARIANT 50 50 K -> R (IN CLONE 2C).	
FT	VARIANT 70 70 MW: A545B149614CF295 CRC64;	
SQ	SEQUENCE 173 AA: 19297 MW;	Score 26.0%; Best Local Similarity 62.2%; Pred. No. 7.9e-30; Matches 84; Conservative 15; Mismatches 34; Indels 2; Gaps 1;
Qy	1 MGTRILCWAAICLLGADHTAAGVSCPTPSNFVTERGKDVFRCDP-SGHFLAYWFRQLGQ 60	Qy 1 MGTRILCWAAICLLGADHTAAGVSCPTPSNFVTERGKDVFRCDP-SGHFLAYWFRQLGQ 60
Db	1 MGTSLLCWWALCLIGADHADTGVSONPRHENITKRGQNTFRCDPISEHNLWYRQLGQ 60	Db 1 MGTSLLCWWALCLIGADHADTGVSONPRHENITKRGQNTFRCDPISEHNLWYRQLGQ 60

QY	61	GPEELIYFOGTTGADDSSGLPNDRFAVRPEGSYSTLKIORTEQGDSAAVLRAGVAAAGWSS	120	RP RX SEQUENCE FROM N.A.
Db	61	GPEELIYFOGNEAQLEKSRLLSRSFSAERPKGFSSTLEIQRTEQGDSAMYLCASSLAGLN-	119	RA RA RA RA RA RT RT RT RL
QY	121	YNEQYFGFGTRITVL	135	"A human T cell-specific cDNA clone encodes a protein having extensive homology to immunoglobulin chains.";
Db	120	-QFHFGDGTTSIL	133	Nature 308:145-149 (1984).
RESULT	7			
TVB7_MOUSE				POTENTIAL.
ID	TVB7_MOUSE	STANDARD;	PRT;	134 AA.
AC	P0320;			T-CELL RECEPTOR BETA CHAIN V REGION YT35.
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-JAN-1988	(Rel. 06, Last sequence update)		
DT	15-JUL-1998	(Rel. 38, Last annotation update)		
DE	T-CELL RECEPTOR BETA CHAIN V REGION CTL F3 PRECURSOR.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	87053852.			
RA	Chou H.S.; Behlik M.A.; Godambe S.A.; Russell J.H.; Brooks C.G., Loh D.Y.;			
RT	"T cell receptor genes in an alloreactive CTL clone: implications for rearrangement and germline diversity of variable gene segments."			
RE	EMBO J. 5:2149-2155 (1986).			
RL	PIR: A02002; RWMBS3.			
DR	PFAM: PF00047; ig; 1.			
KW	T-cell; Receptor; Glycoprotein; Signal.			
FT	SIGNAL	?		
FT	CHAIN	?		
FT	NON_TER	135		
FT	SEQUENCE	135 AA;	135 MW;	9FFB915D33967CC9 CRC64;
Query Match				
Best Local Similarity	50 %	Score 337;	DB 1;	Length 135;
Matches	70;	Conservative	20;	Mismatches 42; Indels 6; Gaps 2;
QY	1	MGTRLLCWAALLGADHTGAGSQTPSNKVTEGRKDVELRCDPISGHATLYWYRQLGQ	60	
Db	1	MDSWTFCCVSCLCILVAKHTDAGVQSPPHEVTEMQEVTLRKPKPSIGHNSLFWYRQTMMR	60	
QY	61	GPEFLIYFGTAGDHSGLPNDREFAVREGSYSTLKIORTEQGDSAYLRAGVAAAGWSS	120	
Db	61	GLELLIYFFNNNVPDDSGAPEDRFSKMPNASFNLKIQSPERDSDAVYF--CASSFST	117	
QY	121	YNEQY--TGPGPTRLV	135	
Db	118	CSANGTYGTSGTRTV	135	
RESULT	9			
TVB1_MOUSE				
ID	TVB1_MOUSE	STANDARD;	PRT;	135 AA.
AC	P01734;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1993 (Rel. 38, Last annotation update)			
DE	T-CELL RECEPTOR BETA CHAIN V REGION 3H.25 PRECURSOR.			
OS	Mus musculus (Mouse)			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	85176939.			
RA	Goverman J.; Minard K.; Shastri N.; Hunkapiller T.; Hansburg D., Sercarz E.; Hood L.;			
RA	"Rearranged beta T cell receptor genes in a helper T cell clone specific for Lysozyme: no correlation between ν beta and MHC restriction."			
RT	RT			
RT	RT			
RL	0.859 867 (1985).			
CC	-!- MISCELLANEOUS: THIS T-CELL CLONE EXPRESSES ONLY A SINGLE ν -BETA CHAIN SEGMENT ALTHOUGH IT HAS THREE REARRANGEMENTS IN THE BETA CHAIN FAMILY.			
CC	-!- MISCELLANEOUS: THIS REARRANGED ν -BETA CHAIN SEGMENT, SPECIFIC FOR CHICKEN ECG-WHITE LYSOZYME AND I-A(B), IS THE SAME AS THAT EXPRESSED IN A T HELPER CELL SPECIFIC FOR CYTOCHROME C AND AN I-E(K) MHC MOLECULE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).			
CC	-----			
CC	DR	M12415; AAA0249.1;		
CC	DR	A02003; RWMBSV.		
DR	PFAM: PF00047; ig; 1.			

CS	Rattus norvegicus (Rat).	SQ	SEQUENCE	133 AA;	14986 MW;	730E9EBF6F85290 CRC64;
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.					
[1]	SEQUENCE FROM N.A.					
RP	SEQUENCE FROM N.A.					
RY	MEDLINE; 87305594.					
RA	"The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";					
RT	Gene 5:75-84 (1987).					
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CC	EMBL; M2521; AAA41420.1; ALT_INIT.					
DR	PIR; B27390; B27390.					
DR	PFAM; PF00047; ig_1.					
DR	PROSITE; PS00290; IG_MHC; 1.					
KW	Immunoglobulin domain; Immunoglobulin C region.					
FT	NON_TER 1					
FT	DISULFID 27 85					
FT	DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).					
FT	SEQUENCE 104 AA; F087906DE45F7276 CRC64;					
QQ	Query Match 10-28; Score 170; DB 1; Length 104;					
Best Local Similarity 41.5%;	Pred. No. 7.8e-08;					
Matches 39; Conservative 12; Mismatches 35;	Indels 8; Gaps 3;					
QQ	144 PEYAVFPESEAFSHTQKATLVCLATGFYDPDVELMSWVNGKEVHSGVSTDPPQLKEQPA 203					
Db	6 PTTVFVPPSTEER-QGNATLKLISDTPSYPSVEAWKANAPISQGVDT-----ANPT 58					
QQ	204 LNDSRYCLSSRRLRVSAFWQNPRNHFRCQVQFYG 237					
Db	59 KQCNKYLASSEFLRATAEWSRS-RNSFICQCVTHEG 91					
RESULT 13						
TVB2_MOUSE	SEQUENCE FROM N.A.					
ID	TVB2_MOUSE					
AC	PO1735;					
DT	21-JUL-1986 (Rel. 01; Created)					
DT	21-JUL-1986 (Rel. 01; Last sequence update)					
DE	T-CELL RECEPTOR_BETA_CHAIN V REGION 86T1 PRECURSOR.					
OS	Mus musculus (Mouse).					
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.					
RN	SEQUENCE STRAIN=BALB/C;					
RC	MEDLINE; 84142271.					
RA	Herrick S.M.; Nielsen E.A.; Kavalier J.; Cohen D.I.; Davis M.M.;					
RT	"Sequence relationships between putative T-cell receptor polypeptides and immunoglobulins."					
RT	Nature 308:153-158(1984).					
DR	PIR; AO004; RMMS8;					
KW	T-cell; Receptor; Glycoprotein; Signal.					
FT	SIGNAL 1 21					
FT	CHAIN 22 133 T-CELL RECEPTOR_BETA_CHAIN V REGION 86T1.					
FT	DOMAIN 22 113 V SEGMENT.					
FT	DOMAIN 114 133 J SEGMENT.					
FT	CARBOHYD 36 36					
FT	CARBOHYD 75 75					
FT	DISULFID 41 109 BY SIMILARITY.					
RESULT 15						
II141_HUMAN	SEQUENCE FROM N.A.					
ID	II141_HUMAN					
PRT;	213 AA.					

AC P15814; 911-08327; Search completed: October 11, 2000, 06:09:24
 DT 01-APR-1990 (Rel: 14, Created)
 DT 01-APR-1990 (Rel: 14, Last sequence update)
 DE 01-OCT-1996 (Rel: 34, Last annotation update)
 DE IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
 GN IGL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1] RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89315835.
 RA Hollis G.P.; Evans R.J.; Stafford-Hollis J.M.; Korsmeyer S.J.;
 RA McTearn J.P.;
 RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
 expressed in pre-B cells and may encode the human immunoglobulin
 omega light-chain protein";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1999).
 [2] RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOID;
 RX MEDLINE: 911-08327.
 RA Evans R.J.; Hollis G.F.;
 RT "Genomic structure of the human Ig lambda 1 gene suggests that it may
 be expressed as an Ig lambda 14.1-like protein or as a canonical B
 cell Ig lambda light chain: implications for Ig lambda gene
 evolution.";
 RL J. EXP. Med. 173:305-311(1991).
 CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
 CC B-CELL LINE (WHICH IS SURFACE Ig NEGATIVE).
 CC -1- MISCELLANEOUS: THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE
 CC IMMUNOGLOBULIN OMEGA LIGHT-CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SHOWS
 CC SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF (J AND C
 CC REGIONS).
 CC DR M27749; AAA56100; 1;
 CC EMBL; M34513; ARA6096; 1;
 CC DR M34511; AAA31096; 1; JOINED.
 CC EMBL; M34512; AAA31096; 1; JOINED.
 CC PIR; A33911; A33911.
 CC DR P01842; 7FAB.
 CC PFAM: PF00047; ig_1.
 CC DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; B-cell; Signal.
 FT SIGNAL 1 ?
 FT CHAIN 213 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
 FT DOMAIN 97 108 J REGION (BY SIMILARITY TO LAMBDA
 FT DOMAIN 109 213 LIGHT-CHAIN.
 FT DOMAIN 109 213 C REGION (BY SIMILARITY TO LAMBDA
 FT DOMAIN 109 213 LIGHT-CHAIN).
 SQ SEQUENCE 213 AA: 22963 MW: 9133A742B9413C79 CRC64;

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 or send an email to license@isb-sib.ch).

 DR M27749; AAA56100; 1;
 DR M34513; ARA6096; 1;
 DR M34511; AAA31096; 1; JOINED.
 DR M34512; AAA31096; 1; JOINED.
 DR PIR; A33911; A33911.
 DR P01842; 7FAB.
 DR PFAM: PF00047; ig_1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; B-cell; Signal.
 FT SIGNAL 1 ?
 FT CHAIN 213 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
 FT DOMAIN 97 108 J REGION (BY SIMILARITY TO LAMBDA
 FT DOMAIN 109 213 LIGHT-CHAIN.
 FT DOMAIN 109 213 C REGION (BY SIMILARITY TO LAMBDA
 FT DOMAIN 109 213 LIGHT-CHAIN).
 SQ SEQUENCE 213 AA: 22963 MW: 9133A742B9413C79 CRC64;

 Query Match 9.6%; Score 160.5; DB 1; Length 213;
 Best Local Similarity 36.6%; Pred. No. 1.2e-06;
 Matches 41; Conservative 18; Mismatches 44; Indels 9; Gaps 5;

 QY 126 FGSPTRILTYLEDIKNVFPPEVAVFEPSEAFIHTOKATLYCLATGFPDHYELSWWNGK 185
 Db 98 FGSGTQIIVLSQLPAT - PSVTFPPSEEL-QANKATLCLMNDPFGITVTVKADGT 154

 QY 186 EVHSGVSTDPOPLIKEQPAINDSEYCLSSRLYSATEHQPNRHERQOQYFG 237
 Db 155 PITQQVEM-TTPSKQ --- SNKYAAASSYSLTPEQWRS-RRSYSCOMHEG 200

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Gencore version 4.5
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OM protein - Protein search, using sw model

Run on: October 11, 2000, 06:08:41 ; Search time 18.52 Seconds
(without alignments)
1583.125 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664

Sequence: 1 MGTRLLCWALCLLGADHTG AVLVSAYVLMAMVKKRDKDSRG 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 9374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_14;*

```
1: sp_archaea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mhc;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rhodet;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	181	10.9	214	11	Q9RIAS	Q9rla5 mus musculus
2	177.5	10.7	259	13	Q9RIAS	Q9rla50 ginglymosto
3	166	10.0	268	13	Q9RIAS	Q9rla54 ginglymosto
4	165.5	9.9	267	13	Q9RIAS	Q9rla529 ginglymosto
5	161	9.7	257	13	Q9RIAS	Q9rla536 ginglymosto
6	156.5	9.4	437	11	Q9RIAS	Q9rla44 mus musculus
7	155.5	9.3	252	13	Q9RIAS	Q9rla46 ginglymosto
8	154	9.3	684	13	Q9RIAS	Q9rla44 ginglymosto
9	146.5	8.8	509	11	Q9RIAS	Q9rla44 ginglymosto
10	145.5	8.7	137	4	Q9UDRL	Q9rla44 ginglymosto
11	145.5	8.7	333	7	Q9RIAS	Q9rla44 ginglymosto
12	145.5	8.7	509	11	Q9WTN4	Q9rla44 mus musculus
13	145	8.7	345	7	P79599	P79599 ratmus norvegicus
14	142.5	8.6	361	7	Q62896	Q62896 ictalus p
15	142	8.5	348	7	Q46815	Q62896 ratmus norvegicus
16	141.5	8.5	237	13	Q9RIAS	Q9rla44 ginglymosto
17	141.5	8.5	346	7	P78088	P78088 ratmus norvegicus
18	141.5	8.5	367	7	P79589	P79589 ratmus norvegicus
19	141	8.5	296	7	Q31274	Q31274 ratmus norvegicus

ALIGNMENTS

RESULT	1	Q9RIAS	PRELIMINARY;	PRT;	214 AA.
ID	Q9RIAS	AC	Q9RIAS;		
DT	01-MAY-2000	(TRIMBLE)	13; Created		
DT	01-MAY-2000	(TRIMBLE)	13; Last sequence update		
DT	01-JUN-2000	(TRIMBLE)	14; Last annotation update		
DE	KAPPA LIGHT-CHAIN OF MAB7 (FRAGMENT).				
OS	Mus musculus (Mouse)				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrv).;				
RT	Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.				
RU	DR EMBL; AF15371; AAD4042.1; -.				
DR	INTERPRO; IPR000495; -.				
DR	INTERPRO; IPR000006; -.				
DR	PFAM; PF00047; iq; 2.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.				
FT	NON_TER 1	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 2	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 3	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 4	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 5	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 6	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 7	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 8	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 9	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 10	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 11	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 12	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 13	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 14	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 15	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 16	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 17	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 18	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 19	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 20	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 21	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 22	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 23	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 24	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 25	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 26	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 27	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 28	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 29	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 30	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 31	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 32	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 33	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 34	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 35	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 36	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 37	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 38	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 39	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 40	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 41	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 42	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 43	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 44	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 45	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 46	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 47	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 48	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 49	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 50	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 51	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 52	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 53	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 54	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 55	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 56	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 57	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 58	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 59	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 60	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 61	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 62	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 63	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 64	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 65	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 66	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 67	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 68	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 69	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 70	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 71	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
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FT	NON_TER 76	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
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FT	NON_TER 81	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 82	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 83	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 84	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
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FT	NON_TER 86	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 87	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 88	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
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FT	NON_TER 92	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 93	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
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FT	NON_TER 96	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 97	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64;
FT	NON_TER 98	214 AA;	214 AA;	214 AA;	23922 MW; 52BA205FDE995E2A CRC64

BIT	Mus musculus (Mouse).	DR	INTERPRO; IPR001039; -.
OS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	INTERPRO; IPR003006; -.
OC	Eukaryota; Metazoa; Chordata; Sciuromorphi; Muridae; Murinae; Mus.	DR	PFAM; PF00047; ig: 1; .
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	PFAM; PF00129; MHC_I; 1; .
RN	[1]	DR	PROSITE; PS00220; IG_MHC; UNKNOWN_1.
RP	SEQUENCE FROM N.A.	KW	MHC.
RC	Sang S.;	FT	NON_TER
RA	"Mouse type III BIT."	SEQUENCE	345 AA; 39221 MW; 9A28E9E36993A7C8 CRC64; .
RT	Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases.	Query Match	8 / 78; Score 145; DB 7; Length 345;
RL	EMBL; AB016184; NRA76555.1; .	Best Local Similarity	22.8%; Pred. No. 1.3e-05;
DR	INTERPRO; IPR00095; -.	Matches	56; Mismatches 104; Indels 84; Gaps 16; .
DR	INTERPRO; IPR003006; -.	Qy	25 QTPSNKVTENGKDVEYLRLRQYDLSVYRSLGGPE 63
DR	PFAM; PF00047; ig: 3; .	Db	63 ETQNAKENEVYRYDLRTRLGYYNQSEGSHSTIOEMYGDDGSLLRGYRDAYGDR 122
DR	PROSITE; PS00220; IG_MHC; UNKNOWN_1.	Qy	25 FLITYFQG--TGAADDGLNDREFAVRPGSVSTLKRQTEQGDS-AAYLRAGVAAGWS 120
SQ	SEQUENCE 509 AA; 55986 MW; CFSASEC9404C14CF CRC64; .	Db	123 YIALNEDLKWTAAAD----FAQ----TRNKWERARYAERLRLQ GTCVEML 168
Query Match	8.7%; Score 145.5; DB 11; Length 509;	Qy	124 YNEQYFGPSTRLTYLEDLKRNVEPPE-VAVFEPSEAEHTOKATLVCLATGFYDPHVEL 178
Best Local Similarity	22.1%; Pred. No. 2e-05;	Db	169 --RRLYLEGETLRSRDPKAHVTLHPREGDV---TLRWALGYPADISL 215
Matches	92; Conservative 56; Mismatches 144; Indels 125; Gaps 22;	Qy	179 SWNTNGKEYHSGSTDPQPIKEQPALNSRYCLSRLRVATEFWQNPRNHRFCQQFYGL 238
Qy	1 MGTRLIC -WAALCL-LGADHTGAGYSQTSPNKVTEKGKDVEYLRCD---PISGHTALY 52	Db	216 SWQINGED---LTQDMELIVETRA-GDGTFRQWASVVVPLGREQN---YTCRVERHEGL 266
Db	11 LGPLLCULLSSCPCTGATGKBLKTQPERSVSAGDSTVLNLTSLLPVG---PIR 67	Qy	239 SENDWTQDRAKPQTQIVSAEANGRADCGFTSESYQGVLSSATIYEILGRATLYNVL 298
Qy	53 WYROSIGQGPFLIYFQGTGA-----ADDGSLPNDRREFAVRPEGSVSTLKIQTREQGD 105	Db	267 PE-----PLSQ-----RWEPLSLDSN---METTVIYVVGAVAIIAAVI 304
Db	68 WYR---GVGSPRLIYSPAGEYVPRTRNSDITKRNMDFSR-----ISNVTPAD 115	Qy	299 SALVLMAMYKRKDSRG 314
Qy	106 SAAYLRAAGVAGWSSYN-EQYQGPGBRLTLEDLKVNFPPEVAVEPSEAFISHPOKATL 164	Db	305 GAVYAVVRRERRNITGG 320
Db	116 AGIYYCYKFQKGSSEPTDQEGGTEVYV---LAKPSPPES---GPADRGIP-DQKVNF 169	RESULT	14
Qy	165 VCATGTFYPDHVELSWAANVKEHV-----SG-----VSTDPPPLKEQPALNSRVC 210	ID	062896 PRELIMINARY; PRT; 361 AA.
Db	170 TCKSHGFSPRNTLKWFKDQELHPLLETTVFFSGKNSYNTSTVRLVLSMDVNSKVIC 229	AC	062896 PRELIMINARY; PRT; 361 AA.
Qy	211 -----LSSRLRVSATE---WQNPRN-----HFRCQ-----VQFYGL 238	DT	01-AUG-1998 (TREMBlrel. 07, Created)
Db	230 EVAHITLDRSPRLRGIANLNSNF-LRVSPVTKVTCQSPSMQVNLTCHAERFYPEDLQLIW 289	DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
Qy	239 SENDWTQDRAKPOTY-----IVSEANWRAADCOT----- 269	DT	01-JUN-2000 (TREMBlrel. 14, Last annotation update)
Db	290 ENGNVSRNDTPPNLTKNDGTWNTSLFLYNSA-HREDVVFTCQVKHDQOPATRNRHTV 348	DE	MHC CLASS I ALPHA CHAIN.
Qy	270 --SESYOOGVL-----SATIYEILLL--KATLYAVLVSALVLMAMYKRKDSRG 314	GN	ICPU-E7.
Db	349 LGFAHSSDQGSMOTFPDNATHNWVFIGVACALLVLLIMAALYLRLRIKKKARG 405	OS	Italuridae punctatus (Channel catfish).
RESULT	13	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterigii; Teleostei; Buteleostei; Ostariophysi; Siluriformes; Italuridae; Italurus.
P79399	SEQUENCE FROM N.A.	RN	[1]
ID	P79599 PRELIMINARY; PRT; 345 AA.	RP	SEQUENCE FROM N.A.
AC	Q9554; .	RA	Antao A.B.; Chinchar V.G.; McConnell T.J.; Miller N.W.; Clem L.W.; Wilson M.R.; .
DT	01-MAY-1997 (TREMBlrel. 03, Created)	RA	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DT	01-MAY-1997 (TREMBlrel. 03, Last sequence update)	RL	EMBL; AF03549; ADD08650; 1; .
DE	DT 2000 (TREMBlrel. 13, Last annotation update)	DR	INTERPRO; IPR001039; -.
DE	MATURE ALPHA CHAIN OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I	DR	INTERPRO; IPR003006; -.
GN	RAT1.	DR	PFAM; PF00047; ig: 1; .
OS	Rattus norvegicus (Rat).	DR	PRODOM; PD000050; -; 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	KW	MHC.
RN	[1]	SEQUENCE	361 AA; 40914 MW; AB686B3F5A9CC1E6 CRC64; .
RP	SEQUENCE FROM N.A.	Query Match	8 / 63; Score 142.5; DB 7; Length 361;
RC	SPAIN=PR1(0); ISSUE=SPLEEN;	Best Local Similarity	25.1%; Pred. No. 2.4e-05;
RA	Joly E., Le Rolle A.F., Gonzalez A.L., Mehling B., Stevens J.,	Matches	32; Mismatches 73; Indels 47; Gaps 7; .
RA	Coddwell W.J., Huening T., Howard J.C., Butcher G.W.; .	Qy	118 WSSNNE-----QYFGGTRLTVLEDIKNVPEPPEAVFEPSEAEISHTQATLYCLAT 169
RA	Curr. Biol. 0:0-01999; .	Db	HSS; P01900; 1BII
RA	EMBL; X80373; CAE62023; .	DR	INTERPRO; IPR00095; -.
RA	INTERPRO; IPR00095; -.	DR	INTERPRO; IPR00095; -; 1; .

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Gencore version 4.5
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OM protein - protein search, using Sw model

Run on: October 11, 2000, 06:08:06 ; Search time 15.62 Seconds
(without alignments)

687,378 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664

Sequence: 1 MGTRLLCWAALCLLGADHTG.....AVLVSALVLMAMVKRKDSRG 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*

1: /SIDSS6/gcqdata/geneseq/geneseqp/AA1980.DAT;*
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4: /SIDSS6/gcqdata/geneseq/geneseqp/AA1983.DAT;*
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6: /SIDSS6/gcqdata/geneseq/geneseqp/AA1985.DAT;*
7: /SIDSS6/gcqdata/geneseq/geneseqp/AA1986.DAT;*
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20: /SIDSS6/gcqdata/geneseq/geneseqp/AA1999.DAT;*
21: /SIDSS6/gcqdata/geneseq/geneseqp/AA2000.DAT;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1664	100.0	314	20 W99374	Human T-cell receptor
2	1433	86.1	314	20 Y15229	Human receptor pro
3	1371	82.4	318	21 Y32208	Human receptor mol
4	1351	81.2	312	21 Y69988	Human receptor-ass
5	1273	76.5	345	21 Y6986	Human receptor-ass
6	1247.5	75.0	311	19 W47589	T-cell receptor be
7	1244	74.8	312	6 P50079	T-cell antigen rec
8	1244	74.8	312	7 P60471	Portion of a human
9	1230	73.9	312	15 R53145	T-cell antigen rec
10	1182	71.0	316	21 Y69999	Human receptor-ass
11	944	56.7	179	21 Y51069	Human TCRbeta prot
12	925.5	55.6	303	20 Y05403	Killer T-cell rece

RESULT 1
W99374 standard; Protein; 314 AA.

ID XX
XX AC W99374;

XX DT 21-MAY-1999 (first entry)

XX DE Human T-cell receptor beta-like protein.

XX KW T-cell receptor beta-like protein; antigen recognition; cancer;

XX KW autoimmune disorder; antagonist; diagnosis.

XX OS Homo sapiens.

XX PN W09903995-A1.

XX PD 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-US14598.

XX PR 18-JUL-1997; 97US-0897097.

XX PA (INCYT) INCYTE PHARM INC.

XX PI Corley NC, Hillman JL;

XX DR WP1; 1999-132239/11.

DR N-PSDB; X25736.

XX PT New isolated T-cell receptor beta-like protein - used to develop products for the diagnosis and treatment of cancer or autoimmune disorders, e.g. AIDS, diabetes, infections or trauma

XX PS Claim 1; Fig 1A-D; 69pp; English.

Human TCRbeta prot	Sequence of T-cell
Sequence encoded by	Mouse A1-T cell re
HTLV-1 Tax/HLA-A2	HLA-A2/flu restric
TCR beta chain and	TCR beta chain and
Mouse H2-DD/flu nu	TCR beta chain and
HLA-A2/IV/gag res	TCR beta chain and
HTLV tax/HLA-A2	TCR beta chain and
Cytotoxic T Lympho	HLA-A2/flu restric
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	Single Chain T cell
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
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Mammalian T Lympho	TCR beta chain and
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Marine cytotoxic T	TCR beta chain and
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Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	TCR beta chain and
Marine cytotoxic T	TCR beta chain and
Human TCRbeta prot	TCR beta chain and
Sequence of the be	TCR beta chain and
Mammalian T Lympho	TCR beta chain and
Cytotoxic T Lympho	

XX This sequence represents a new purified T-cell receptor (TCR) beta-like
 CC protein (TCRLP). The TCRLPs are essential to the formation of a
 CC functional TCR and play a role in antigen recognition by T cells.
 CC The TCRLP polypeptides and polynucleotides appear to play a role in
 CC cancer and autoimmune disorders. The TCRLP and agonists can be used for
 CC treating cancer. TCRLP antagonists can be used for treating autoimmune
 CC disorders, e.g. AIDS, Addison's disease, adult respiratory distress
 CC syndrome, allergies, anaemia, asthma, atherosclerosis, bronchitis,
 CC cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis,
 CC dermatomyositis, diabetes mellitus, erythema nodosum, atrophic
 CC gastritis, glomerulonephritis, gout, Graves' disease, hypersensitivity,
 CC irritable bowel syndrome, lupus erythematosus, multiple sclerosis,
 CC myasthenia gravis, myocardial or pericardial inflammation, osteoporosis,
 CC osteoarthritis, pancreatitis, polymyositis, rheumatoid arthritis,
 CC scleroderma, Sjogren's syndrome, and autoimmune thyroiditis,
 CC complications of cancer, haemodialysis, and extracorporeal circulation,
 CC viral, bacterial, fungal, parasitic, protozoal, and helminthic infections
 CC and trauma. The products can also be used for detection, diagnosis and
 CC drug screening.
 XX Sequence 314 AA;

Query Match 100.0%; Score 1664; DB 20; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2.4e-144;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKTYEKGRDVELRDPISGHTALYWYROSQGQ 60

Db 1 mgtrllcwaalcilgadhtgaaqtqsnkvtkegdkvelrcdpisghtalywqslqq 50

Oy 61 GPBFLIVFOGTGAADDGGLPNDRFAVRPEEGGVSTIKIORTPEQGDSAYLRAGVAGWSS 120

Db 61 gpbfliyfgtgaaaddgglpndrfavrpeeggvstikiqregqsdasaylragvagwss 120

Oy 121 YNBOYFGFGTRTLVLEDIKNVYPPPEAVFEPSEAEISHTOKATLYSLATGFYPDFHVELSW 180

Db 121 ymeyqfgrgtrtlvediknvpppeavfeppeaeishtqpatlivelatgypdihelsw 180

Oy 181 WNGKEYHSGVSTDQPLIKEQDALNDSYCLSRLIVSATWQNPNHFCQVQYGLSE 240

Db 181 wngkeyhsqvstdqplikeqdalsndsyclsrlivsatwqnprnhfcqvcqyqise 240

Oy 241 NDIWTQDRAKPTQIVSAEAWSGRADCFTSESYQQGVLSATILYELIGLIGATLYAVLVSA 300

Db 241 ndewtqdrakptqivsaewgradgftssyqqgvlsatillyeilgkatzlyavlvsa 300

Oy 301 LVIMAMYKRKDSSG 314

Db 301 lv_imam_ykrkdssg 314

RESULT 2
 Y15229 ID Y15229 standard; protein; 314 AA.

XX Homo sapiens.

AC Y15229;

DT 26-OCT-1999 (first entry)

XX Human receptor protein (HURP) 8 amino acid sequence.
 KW receptor; cancer; autoimmune disorder; inflammation;
 KW antagonist; cell surface protein; cell signalling;
 KW antibody; human receptor protein; HURP; reproductive disorder;
 KW developmental disorder; gastrointestinal disorder.

OS Homo sapiens.

XX Location/Qualifiers

Key 205

FT /note= "Potential N-glycosylation site"

XX	FT	Misc-difference 312	/note= "Potential CAMP-/cGMP-dependent protein-kinase phosphorylation site"
CC	FT	Misc-difference 101	/note= "Potential casein kinase II-phosphorylation site"
CC	FT	Misc-difference 133	/note= "Potential casein kinase III-phosphorylation site"
CC	FT	Misc-difference 152	/note= "Potential casein kinase III-phosphorylation site"
CC	FT	Misc-difference 239	/note= "Potential casein kinase III-phosphorylation site"
CC	FT	Misc-difference 26	/note= "Potential protein kinase C-phosphorylation site"
CC	FT	Misc-difference 81	/note= "Potential protein kinase C-phosphorylation site"
CC	FT	Misc-difference 95	/note= "Potential protein kinase C-phosphorylation site"
CC	FT	Misc-difference 159	/note= "Potential protein kinase C-phosphorylation site"
CC	FT	Misc-difference 212	/note= "Potential protein kinase C-phosphorylation site"
XX	XX	WO991375-A2.	
XX	XX	PN 19-AUG-1999.	
XX	XX	XX 05-FBB-1999;	99WO-US05572.
XX	XX	PR 12-FBB-1998;	98US-0022939.
XX	XX	XX (INCY) INCYTE PHARM INC.	
XX	XX	XX Au-Young J, Bandman O, Baughn M, Corley NC, Guegler KJ;	
XX	XX	XX Hillman JL, Tal P, Shah P, Tang YT, Yue H;	
XX	XX	XX WPI: 1999-494536/41.	
XX	XX	XX DR N-PSDB; 206373.	
XX	XX	XX New human receptor proteins, used e.g. to treat, prevent and diagnose gastrointestinal and developmental disorders - and related nucleic acids, vectors, transformed cells, antibodies, agonists and antagonists	
XX	PS	XX Claim 1; Page 85-86; 94pp; English.	
XX	XX	XX The Human receptor protein 8 (HURP-8) shares 87% identity with human T-cell receptor beta.	
CC	CC	CC HURP-8 is expressed in cancerous, inflamed, haematopoietic/immune and gastrointestinal tissue. HURP-4 therefore appears to have a role in some forms of cancer, inflamed, haematopoietic/immune and gastrointestinal disorders.	
CC	CC	CC This gives rise to the possibility of using an antagonist or an antibody of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.	
XX	XX	XX Sequence 314 AA;	
XX	XX	XX Query Match 86.1%; Score 1433; DB 20; Length 314;	
CC	CC	CC Best Local Similarity 86.6%; Pred. No. 3.1e-123;	
CC	CC	CC Matches 272; Conservative 12; Mismatches 30; Indels 0; Gaps 0;	
QY 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKTYEKGRDVELRDPISGHTALYWYROSQGQ 60	Db 1 mgtrllcwaalcilgadhtgaaqtqsnkvtkegdkvelrcdpisghtalywqslqq 60		

CC tumours, uterine fibroids, autoimmune disorders, ectopic pregnancy,
 CC teratogenesis, breast cancer, fibrocystic breast disease,
 CC galactorrhoea, disruptions of spermatogenesis, abnormal sperm
 CC physiology, testis cancer, prostate cancer, benign prostatic
 CC hyperplasia, prostatitis, Peyronie's disease, male breast carcinoma
 CC and gynaecomastia; gastrointestinal disorders including, but are not
 CC limited to, dysphagia, Peptic oesophagitis, oesophagitis, abdominal spasm and
 CC stricture, oesophageal carcinoma, dyspepsia, indigestion, gastritis,
 CC gastric carcinoma, anaesthesia, nausea, gastrroparesis, intestinal
 CC tract infection, peptic ulcer colitis, Whipple's disease, Mallory-Weiss
 CC syndrome, irritable bowel syndrome, short bowel syndrome, diarrhoea,
 CC constipation, cirrhosis, jaundice, and hepatic vein thrombosis; nervous
 CC disorders including, but are not limited to, Alzheimer's disease,
 CC amnesia, bipolar disorder, catatonia, cerebral neoplasms, Down's
 CC syndrome, and dystonia; smooth muscle cell disorders including, but
 CC not limited to, angina, anaphylactic shock, arrhythmia, cardiovascular
 CC shock, migraine, and pheochromocytoma; musculoskeletal disorders
 CC including muscular dystrophy, lipid myopathy, inclusion body myositis,
 CC centronuclear myopathy, lipiodol myopathy, inclusion body myositis,
 CC thyrotoxic myopathy, and ethanol myopathy; immunological disorders
 CC including AIDS, Addison's disease, adult respiratory distress
 CC syndrome, allergy, ankylosing spondylitis, amyloidosis, anaemia,
 CC asthma, atherosclerosis, autoimmune hemolytic anaemia, autoimmune
 CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
 CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
 CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
 CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's
 CC syndrome, systemic lupus erythematosis, systemic sclerosis, glomerulonephritis,
 CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
 CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
 CC myasthenia gravis, myocardial or pericardial inflammation,
 CC DE osteoporosis, episodic lymphopenia with lymphocytotoxins, erythroblastosis
 CC AC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,
 CC XX Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
 CC DT DT 15-FEB-2000 (first entry)
 CC DE Human receptor molecule (REC) encoded by Incyte clone 3428945.
 CC XX Receptor: RAC; human; diagnosis; therapy; neoplastic disorder;
 CC KW immunological disorder; reproductive disorder; nervous disorder;
 CC KW gastrointestinal disorder; smooth muscle disorder;
 CC KW musculoskeletal disorder.
 CC XX Homo sapiens.
 CC XX WO957270-A2.
 CC PN PD 11-NOV-1999.
 CC XX PF 28-APR-1999; 99WO-US09191.
 CC XX PR 01-MAY-1998; 98US-0071822.
 CC PA (INCYT) INCYTE PHARM INC.
 CC PI Hillman JL, Bandman O, Tang YT, Yue H, Lal P, Corley NC;
 CC PI Guegler KJ, Patterson C;
 CC XX DR WPI: 2000-052971/04.
 CC DR N-PSDB: 2346LT.
 CC XX Novel human receptor molecules used in the diagnosis, treatment and
 PT prevention of neoplastic, immunological, reproductive, gastrointestinal,
 PT nervous, smooth muscle and musculoskeletal disorders -
 XX Claim 1; Page 80-81; 94pp; English.
 PS XX The present sequence represents a human receptor molecule (REC)
 CC encoded by Incyte cDNA clone 3428945. The invention provides human
 CC RECs and polynucleotides which identify and encode REC, as well as
 CC vectors, host cells, antibodies, agonists and antagonists. Human
 CC RECs appear to play a role in neoplastic, immunological,
 CC reproductive gastrointestinal, nervous, smooth muscle and
 CC musculoskeletal disorders. The protein, antagonists and agonists,
 CC and compositions can be used to treat: a) reproductive disorder,
 CC infertility including tubal disease, ovulatory defects, endometriosis,
 CC disruptions of the oestrous and menstrual cycles, polycystic ovary
 CC syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian

CC tumours, uterine fibroids, autoimmune disorders, ectopic pregnancy,
 CC teratogenesis, breast cancer, fibrocystic breast disease,
 CC galactorrhoea, disruptions of spermatogenesis, abnormal sperm
 CC physiology, testis cancer, prostate cancer, benign prostatic
 CC hyperplasia, prostatitis, Peyronie's disease, male breast carcinoma
 CC and gynaecomastia; gastrointestinal disorders including, but are not
 CC limited to, dysphagia, Peptic oesophagitis, oesophagitis, abdominal spasm and
 CC stricture, oesophageal carcinoma, dyspepsia, indigestion, gastritis,
 CC gastric carcinoma, anaesthesia, nausea, gastrroparesis, intestinal
 CC tract infection, peptic ulcer colitis, Whipple's disease, Mallory-Weiss
 CC syndrome, irritable bowel syndrome, short bowel syndrome, diarrhoea,
 CC constipation, cirrhosis, jaundice, and hepatic vein thrombosis; nervous
 CC disorders including, but are not limited to, Alzheimer's disease,
 CC amnesia, bipolar disorder, catatonia, cerebral neoplasms, Down's
 CC syndrome, and dystonia; smooth muscle cell disorders including, but
 CC not limited to, angina, anaphylactic shock, arrhythmia, cardiovascular
 CC shock, migraine, and pheochromocytoma; musculoskeletal disorders
 CC including muscular dystrophy, lipid myopathy, inclusion body myositis,
 CC centronuclear myopathy, lipiodol myopathy, inclusion body myositis,
 CC thyrotoxic myopathy, and ethanol myopathy; immunological disorders
 CC including AIDS, Addison's disease, adult respiratory distress
 CC syndrome, allergy, ankylosing spondylitis, amyloidosis, anaemia,
 CC asthma, atherosclerosis, autoimmune hemolytic anaemia, autoimmune
 CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
 CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
 CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
 CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's
 CC syndrome, systemic lupus erythematosis, systemic sclerosis, glomerulonephritis,
 CC Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
 CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
 CC myasthenia gravis, myocardial or pericardial inflammation,
 CC DE osteoporosis, episodic lymphopenia with lymphocytotoxins, erythroblastosis
 CC AC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,
 CC XX Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
 CC DT DT 15-FEB-2000 (first entry)
 CC DE Human receptor molecule (REC) encoded by Incyte clone 3428945.
 CC XX Receptor: RAC; human; diagnosis; therapy; neoplastic disorder;
 CC KW immunological disorder; reproductive disorder; nervous disorder;
 CC KW gastrointestinal disorder; smooth muscle disorder;
 CC KW musculoskeletal disorder.
 CC XX Homo sapiens.
 CC XX WO957270-A2.
 CC PN PD 11-NOV-1999.
 CC XX PF 28-APR-1999; 99WO-US09191.
 CC XX PR 01-MAY-1998; 98US-0071822.
 CC PA (INCYT) INCYTE PHARM INC.
 CC PI Hillman JL, Bandman O, Tang YT, Yue H, Lal P, Corley NC;
 CC PI Guegler KJ, Patterson C;
 CC XX DR WPI: 2000-052971/04.
 CC DR N-PSDB: 2346LT.
 CC XX Novel human receptor molecules used in the diagnosis, treatment and
 PT prevention of neoplastic, immunological, reproductive, gastrointestinal,
 PT nervous, smooth muscle and musculoskeletal disorders -
 XX Claim 1; Page 80-81; 94pp; English.
 PS XX The present sequence represents a human receptor molecule (REC)
 CC encoded by Incyte cDNA clone 3428945. The invention provides human
 CC RECs and polynucleotides which identify and encode REC, as well as
 CC vectors, host cells, antibodies, agonists and antagonists. Human
 CC RECs appear to play a role in neoplastic, immunological,
 CC reproductive gastrointestinal, nervous, smooth muscle and
 CC musculoskeletal disorders. The protein, antagonists and agonists,
 CC and compositions can be used to treat: a) reproductive disorder,
 CC infertility including tubal disease, ovulatory defects, endometriosis,
 CC disruptions of the oestrous and menstrual cycles, polycystic ovary
 CC syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian

Query Match 3
 Best Local Similarity 82.4%; Score 1371; DB 21; Length 318;
 Matches 265; Conservative 11; Mismatches 37; Indels 6; Gaps 2;

Qy 1 MGTRLLCWAALCLLG --- ADHTGAGVSSTPSNKVTEKGKDVELRCDPISGHITALYNNR 55
 Db 1 mgtsllcwwvlgflgtdsvtstdtgagsgsprkvtk9qdtvtlrcdpsshatlyyyq 60

Qy 56 QSLGQCPFLIFQSTGAADDGLPNDRFAVRPGSVSPLKIRTEQGDSAAVLRAGYA 115
 Db 61 galggppfityfnveapqdksgipsdrfsaerpssisltqteqrdsamy-reass 119

Qy 116 AGWSSNEOYFGPGPRLTYLEDLKAVFPPPEVAFPSAEFISHOTKATLGFYPPDH 175
 Db 120 latggteifglfegslltyleldlkivfppeavafpseseaishtcqktlvclatgypoh 179

Qy 176 VELSWWNGKEVHSGVSTDQPLIKEOPALNDRYCLSRLRVSAFENPNRHFRCOQF 235
 Db 180 velswwngkevhsgvstdqplikeopalndryclsrlrvsafrqpnhrfcqyqf 239

Qy 236 YGLSENDEWTQDRAFPVTQIVSAEANGRADCGFTSESYQQGVLSATILEBILSKATLYA 295
 Db 240 yglsendewqdralptqivsaawgradicftsesyqgvlsatiljeillgkatiya 299

Qy 296 VLVALVLMAMVKRDGR 314
 Db 300 vlvslvalvlmamvkrdgr 318

RESULT	4							
Y69988								
ID	Y69988	standard; protein;	312 AA.					
XX								
AC	Y69988;							
XX								
DT	31-MAY-2000	(first entry)						
XX								
DE	Human receptor-associated protein from Incyte clone 2907954.							
XX								
KW	Human receptor-associated protein; HRAP; Incyte Clone 2907954; cytostatic; immunomodulatory; antiinflammatory; cardiotropic; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic; antirheumatic; antiasthmatic; osteoprotective; neuroprotective; treatment; reproductive; cell proliferative; autoimmune/inflammatory disorders (e.g. atherosclerosis, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome).							
XX								
OS	Homo sapiens.							
XX								
FH	Key	Location/Qualifiers						
FT	Modified-site	26	/note= "Potential phosphorylation site"					
FT	Modified-site	37	/note= "Potential phosphorylation site"					
FT	Modified-site	95	/note= "Potential phosphorylation site"					
FT	Modified-site	114	/note= "Potential phosphorylation site"					
FT	Modified-site	131	/note= "Potential phosphorylation site"					
FT	Modified-site	150	/note= "Potential phosphorylation site"					
FT	Modified-site	157	/note= "Potential phosphorylation site"					
FT	Modified-site	210	/note= "Potential phosphorylation site"					
FT	Modified-site	237	/note= "Potential phosphorylation site"					
FT	Modified-site	237	/note= "Potential phosphorylation site"					
FT	Modified-site	203	/note= "Potential N-glycosylation site"					
XX								
PN	WO200008155-A2.							
XX								
PD	17-FEB-2000.							
XX								
PF	06-AUG-1999;	99WO-US177777.						
XX								
PR	07-AUG-1998;	98US-0160065.						
PR	01-SEP-1998;	98US-0098703.						
XX								
PA	(INCYT) INCYTE PHARM INC.							
XX								
PI	Hillman JL, Yue H, Lal P, Corley NC, Baughn MR;	Tang YT, Gorgone GA, Guegler KJ,						
XX								
DR	WPI: 2000-205710/18.							
DR	N-PSDB; 250880.							
XX								
PT	New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders.							
PT								
XX								
PS	Claim 1; Page 75; 99pp; English.							

The present sequence is a human receptor-associated protein (HRAP) from Incyte clone 2907954 obtained from THYMN005 cDNA library. This sequence is expressed in haemopoietic/immune, gastrointestinal, and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiotropic, antiarteriosclerotic, hepatotropic, antiarthritic, antidiabetic, dermatological, antiasthmatic, osteoprotective, activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory disorders (e.g. atherosclerosis, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome).

Query Match Score 81.2%; Best Local Similarity 83.0%; Pred. No. 9.8e-116; Matches 264; Conservative 12; Mismatches 32; Indels 10; Gaps 2; Sequence 312 AA;

Query Match Score 81.1%; Best Local Similarity 83.0%; Pred. No. 9.8e-116; Matches 264; Conservative 12; Mismatches 32; Indels 10; Gaps 2;

Qy 1 MGTRLLCWAAILCLIGADHTAGVQSOTPSNKYTERGKDYBLRCDPISGHATLYWYRQSLGQ 60

Db 1 mgtrllcwaailcligadhtagvqsotpsnktytergkdyblrcdpisghatlywyrqslgq 60

Qy 61 GPEFLIYFQGTGAADDGGILPNDRFFAVRPEGSYSTKLQIRTEQGDSAAYLRAGVAAAGNS 120

Db 61 gpkliliqfqnngvvdsqqpkdrsaerklgvdstiklakedsavica-----ss 114

Qy 121 Y----NEQYFGPGTILTVLEDIKNVFPBPVYAEVPSEASITISHRPOKATLYCLANGFYPHV 176

Db 115 fidroneqfpggritrllediknvfppeavfcpseasishcqkvlcqfphv 174

Qy 177 ELSWWNGKEVHSGYSTDOPILKEPALNDSYCLSSRRVSVATFWQFNHRPCQYFY 236

Db 175 elswwwngkevhsgrystdpilkepalndsrlyssrrvsvafwqprnhrcqrqfy 234

Qy 237 GLSENDEWTODRAKEVTQIVSAEAWGRADGETSESYOGVLSNTILEYLIGRATIYAV 296

Db 235 qlsendewtqdrukptqivsaaewgradctfsesyygvlsatilyeilgkatiyav 294

Qy 297 LYSALVLMANKVRKDSRG 314

Db 295 lvsalvlmankvrkdsrg 312

RESULT 5

ID Y69986 standard; Protein; 345 AA.

XX

XX

AC Y69986;

XX

XX

DE Human receptor-associated protein from Incyte clone 1877651.

XX

XX

Human receptor-associated protein; HRAP; Incyte clone 1877651;

KW cytostatic; immunomodulatory; antiinflammatory; cardiotropic; antiarteriosclerotic; hepatotropic; antiarthritic; antidiabetic; dermatological; antiasthmatic; osteoprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune/allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.

XX

Homo sapiens.

XX

XX

Human receptor-associated protein; HRAP; Incyte clone 1877651;

KW cytostatic; immunomodulatory; antiinflammatory; cardiotropic; antiarteriosclerotic; hepatotropic; antiarthritic; antidiabetic; dermatological; antiasthmatic; osteoprotective; diagnosis; treatment; prevention; reproductive disorder; cardiovascular; cell proliferative; autoimmune/allergy; gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS; arthritis; anemia; asthma; dermatitis; diabetes; osteoporosis; multiple sclerosis; irritable bowel syndrome.

XX

OS

XX

FH

FT Key Modified-site 32

FT Location/Qualifiers

FT /note= "Potential phosphorylation site"

FT 164

FT Modified-site

FT

Db	178 wngkevhsgvstdppalpkecpalndsrclssrrvsatfwgnprnhfrccqfqyqse 237	Db	178 lswwngkevhsgvstdppalpkecpalndsrclssrrvsatfwgnprnhfrccqfqyf 237
Qy	241 NDEWTODRAKPTQIVSAEAWGRADCGFTSESSQQGVLSATILYEILLGKATLYAVLVA 300	Qy	238 LSENDEWTOQDRAKPTQIVSAEAWGRADCGFTSESSQQGVLSATILYEILLGKATLYAVL 297
Db	238 ndewtqdrakptqivsaewgradcgftseyyqqgvlsatilyeillgkattyavla 297	Db	238 lsendewtqdrakptqivsaewgradcgftsvsyqqgvlsatilyeillgkattyav 297
Qy	301 LVLMAMYKRKDSRG 314	Qy	298 VSALVLMAMYKRKD 311
Db	298 lvlmamvkrkdsrg 311	Db	298 vsalvlmamvkrkd 311
RESULT 7		RESULT 8	
P50079	ID P50079 standard; protein: 312 AA.	P60471	ID P60471 standard; Protein: 312 AA.
XX	XX	XX	XX
AC		AC	
XX		XX	
DT 19-MAR-1992	(first entry)	DT 13-JUN-1991	(first entry)
XX		XX	
DE T-cell antigen receptor protein.		DE Portion of a human T-cell antigen receptor protein.	
XX		XX	
KW T-cell receptor; DNA probe; tumor marker; ss.		KW Cancer; tumour cell; T-cell receptor.	
XX		XX	
PN EP14958-A.		OS Homo sapiens.	
XX		XX	
PD 24-JUL-1985.		PN CA197488-A.	
XX		XX	
PF 14-JAN-1985;	85EP-0300243.	PD 03-DEC-1985.	
XX		XX	
PR 06-FEB-1984;	84US-0577556.	PF 01-FEB-1984;	84CA-0446545.
XX		XX	
PA (ONTA-) ONTARIO CANCER INST.		PR 01-FEB-1984;	84CA-0446545.
XX		XX	
PI Mak TW		PA (ONTA-) ONTARIO CANCER INST.	
XX		XX	
DR WPI:1985-179193/30.		PI Mak TW;	
XX		XX	
N-PSDB; N50091.		DR WPI:1996-002147/02.	
PT New nucleic acid encoding T-cell antigen receptor polypeptide -		DR N-PSDB; N60466.	
PT useful for prepn. of probes or antibodies for detection of		PT New pure nucleic acid with sequence encoding T-cell polypeptide	
PT tumour cells and T-cells		PT is prep'd. by recombinant DNA methods for use as probe when	
XX		PT labelled and for antibody prodn.	
PS Disclosure; Fig 3; 15pp; English.		XX	
XX		PS Claim 4; Fig 3; 22pp; English.	
CC This protein resembles human and mouse Ig light chain		XX	
CC molecules. This protein is encoded by clone YT35 and is		CC Receptor protein product has at least 60% homology with the clone YT	
CC part of the antigen receptor mediating specialized T-		CC 35. The product resembles human and mouse Ig light chain molecules,	
CC lymphocyte function. Antibodies may be directed against		CC and may be labelled for use as a probe for the detection of the	
CC this protein and used for detection of T-cell receptor		CC T-cell receptor antigen, and identification of unknown (esp. tumour	
CC antigen so that unknown cells, e.g. a tumor cell, can be		CC cells) as T-cells.	
XX		XX	
SQ Sequence 312 AA;		SQ Sequence 312 AA;	
Query Match 74.8%; Score 1244; DB 6; Length 312;		Query Match 74.8%; Score 1244; DB 7; Length 312;	
Best Local Similarity 77.1%; Pred. No. 5.9e-106;		Best Local Similarity 77.1%; Pred. No. 5.9e-106;	
Matches 242; Conservative 21; Mismatches 45; Indels 6; Gaps 2;		Matches 242; Conservative 21; Mismatches 45; Indels 6; Gaps 2;	
Qy 1 NGTRLLCWAALLLGADHHCAGVSOPSNKVTKRDKDVELRCDPISGHFTALYWRQLGQ 60		Qy 1 MGTRLLCWAALLLGADHHCAGVSOPSNKVTKRDKDVELRCDPISGHFTALYWRQLGQ 60	
Db 1 mdswtfcvscilvakhtdagvicsprnevtengqvtlrcqpsqnslfyrgtmmr 60		Db 1 mdswtfcvscilvakhtdagvicsprnevtengqvtlrcqpsqnslfyrgtmmr 60	
Qy 61 GPEFLIYFQGTGAADDGLPNDRFFAVPRPEGSVSTLKIRTEGDSAAAYLRAGYAAGRSS 120		Qy 61 GPEFLIYFQGTGAADDGLPNDRFFAVPRPEGSVSTLKIRTEGDSAAAYLRAGYAAGRSS 120	
Db 61 gielillynnnypiddsgmepdrfsakmpnasflstikqippeprisavyf---cassifst 117		Db 61 gielillynnnypiddsgmepdrfsakmpnasflstikqippeprisavyf---cassifst 117	
Qy 121 YNEQY--FGPGTRLTYLEDKINKEPEPEAVEPESEAISHTOKATLYCLATGFYPDHYE 177		Qy 121 YNEQY--FGPGTRLTYLEDKINKEPEPEAVEPESEAISHTOKATLYCLATGFYPDHYE 177	
Db 118 csanyytfgsgrtrtvedinkvfpevavtseaeishgtatgvciatgfpdive 177		Db 118 csanyytfgsgrtrtvedinkvfpevavtseaeishgtatgvciatgfpdive 177	
Qy 178 LSWWNGKEYHSGYSTDPOPIIKEQPALNDRSRYCLSSRLRVSATENONPRHFRFCQYQFYG 237		Qy 178 LSWWNGKEYHSGYSTDPOPIIKEQPALNDRSRYCLSSRLRVSATENONPRHFRFCQYQFYG 237	

Db	178 lswwvngkevhsgvstcpaplkpealndsrccssrlrvsatwqnprmhfrcqvfqyf	237	Qy 121 YNEQY--FPGPTRLTIVDELKNYPPEAVFEPSEAEISHTQATLVLCLATGFYFPDHYE 177	Db 118 csanygtfsgrtrivvedinkvppeavfepseaeishtqatlvclatgfipdhye 177
Qy	238 LSENDENTODRAKPTQIVSYAEEANGRADCGFTISESYQQGVSATLYEILGLKATLYAVL	297	Db 178 LSWWYNGKEYHSGVSTDQPLKEQALANDSRCCSRLRVSATWMQNPRAHFRCOVQFYG 237	
Db	238 lsendentodraakptqivsaaegradeftsvyggvsatlyeilglkatiyavl	297	Qy 178 lswwrkgkehsqgstdpqlkeqalndsrccsrlrvsatqnpnhrfrcqfqyf 237	
Qy	298 VSALVLMAMYKRKD 311		Db 238 LSENDENTODRAKPTQIVSAEANGRADCGFTSESYQQGVLSATLYEILGLKATYAVL 297	
Db	298 vsalvlmamymkrkd 311		Qy 238 lsendentodraakptqivsaaegradeftsvyggvsatlyeilglkatiyavl 297	
RESULT 9			Db 238 lsendentodraakptqivsaaegradeftsvyggvsatlyeilglkatiyavl 297	
R53145	ID R53145 standard; Protein; 312 AA.		Qy 298 VSALVLMAMYKRKD 311	
XX	DE		Db 298 vsalvlmamymkrkd 311	
R53145;	XX			
AC	XX			
	XX			
DT	08-SEP-1994 (first entry)			
XX	XX			
T-cell antigen receptor.	DE			
XX	XX			
T-cell antigen receptor; T-lymphocyte; probe; hybridization; MOLT-3.	KW			
XX	XX			
Homo sapiens.	OS			
XX	XX			
Key Location/Qualifiers	FH			
Misc-difference 90	FT			
Misc-difference /note= "Possible N-glycosylation site"	FT			
Misc-difference 205	FT			
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XX	XX			
EP593092-A..	FN			
20-APR-1994.	XX			
PD	XX			
14-JAN-1985;	PP			
XX	XX			
PR 13-JAN-1984;	PR			
PR 06-FEB-1984;	PR			
XX	XX			
(ONTA-) ONTARIO CANCER INST.	OS			
XX	XX			
PI Mak TW;	PH			
XX	FT			
DR WPI: 1994-127936/16.	FT			
DR N-PSDB; Q62128.	FT			
XX	FT			
New nucleic acid encoding T-cell antigen receptor - is useful	PT			
PT e.g. as a probe to identify T-cells	PT			
XX	FT			
Disclosure: Fig 3; 13pp; English.	PS			
XX	FT			
CC mRNA complementary to the DNA sequence given in Q62128 is obtained by	FT			
CC isolating mRNA from MOLT-3 cells, preparing cDNA, inserting the cDNA	FT			
CC into the BIIIB site of vector pPP50CEB5, transfecting the vector into	FT			
CC Escherichia coli HB101, and screening for 1.3 kb T-cell specific	FT			
CC mRNA in MOLT-3 and HSC-58 cells. The mRNA encodes a portion of the	FT			
CC T-cell antigen receptor (sequence R53145).	FT			
XX	FT			
Sequence 312 AA;	SQ			
Query Match Score 1230; DB 15; Length 312;				
Best Local Similarity 76.8%; Pred. No. 1.1e-104;				
Matches 241; Conservative 21; Mismatches 46; Indels 6; Gaps 2;				
Qy 1 MGTRLLWAALCLIGADHTAGVGSQTPSNKTYEKGDFVELRCDPISGHATLYWYROSQG 60				
Db 1 mdswtccsicilvkhdtaviprhrhvemqevtrckpishnsifsyrgmm 60				
Qy 61 GPEFLIYFQGCTGAADDGLPNDREFAYPRPEVSSTIKIQRTEQGDSAAYLRAGVAGWS 120				
Db 61 qlelllfyffnnyyridscomoeoqrdfkkmponsfslkknocoreoasavf---cassps 117				

FT	Modified-site	76	/note= "N-glycosylation site"	Qy	295 AVLYSALVLMAMVKKDKDSRG 314
FT	Modified-site	89	/note= "N-glycosylation site"	Db	297 avlysalvlmamvkkdkdsrg 316
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FT	XX			Y51069	
PN	WO200008155-A2.			ID Y51069 standard; protein; 179 AA.	
XX				XX	
PD	17-FEB-2000.			AC Y51069;	
XX				XX	
PF	06-AUG-1999;	99WO-US17777.		DT 22-MAR-2000 (first entry)	
XX				XX	
PR	07-AUG-1998;	98US-0160065.		DE Human TCRbeta protein fragment #2.	
PR	01-SEP-1998;	98US-0098703.		XX	
XX				KW T cell receptor beta; TCRbeta; human; constant region; immunosuppressor.	
PA	(INCY) INCYTE PHARM INC.			XX	
XX				OS Homo sapiens.	
PI	Hillman JL, Yue H, Lai P, Tang YT, Gorgone GA, Guegler KJ;			XX	
PI	Corley NC, Baugn MR;			JP11302299-A.	
XX				XX	
DR	WPI: 2000-205710/18.			PN 02-NOV-1999.	
DR	N-PSDB; Z50901.			XX	
XX				PP 21-APR-1998; 98JP-0110607.	
PT	New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders -			XX	
PT	WPI: 2000-205710/18.			PR 21-APR-1998; 98JP-0110607.	
XX				XX	
PS	Claim 1; Page 86; 9pp; English.			PA (KIRIN) KIRIN BREWERY KK.	
XX				XX	
CC	The present sequence is a human receptor-associated protein (HRAP) from Incyte clone 2656082 obtained from THYMOT04 cDNA library.			DR WPI: 2000-075345/07.	
CC	This sequence is expressed in haematopoietic/immune, gastrointestinal and reproductive tissues. HRAP has cytosstatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiasthmatic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome).			XX	
CC				PT T cell receptor beta chain constant region peptide - has immunosuppressing activity	
CC				PS Claim 4; Page 12-13; 15pp; Japanese.	
CC				XX	
CC				CC This invention describes a novel polypeptide comprising substantially part or all of the constant region of T cell receptor beta chain (TCRbeta) and containing substantially no other regions of TCRbeta and having immunosuppressing activity. The TCRbeta requires no consideration of tissue-compatible antigen for the patient to be dosed nor of antigen specificity. This sequence represents a fragment of the human TCRbeta protein described in the method of the invention.	
CC				CC Sequence 179 AA:	
CC				XX	
SQ	Sequence 316 AA;			Query Match Score 94%; DB 21; Length 179;	
				Best Local Similarity 100.0%; Pred. No. 7_5e-79;	
				Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MGRLLGWAALLGGADHTGAGGSQTPSNKVTEKGRDKDVELRCDPISGHATAWYRQSLGQ 60		3;	Qy 136 EDLRNVFPPEAVAFEPSSAEISHTQATLVEIATGFDPDHVELSWANGKEYHSGVYSTDP 195	
Db	1 mgcrllicavclllgavpmegvtq.prlymgmtnkkslcgehlgnamykqsakk 60			Db 1 edlrvnfppeavafepssaeishtqatlvatgfdpdhvelswangkeyhsgvstdp 60	
Qy	61 GPEFLIYFGTGAADDGSLPNDFFAVRPEGSVSTLIKQTEOGDSAAYLRA-----GV 114			Qy 196 QPLKEQPALNDSRCLSSRLRVATFVNPNRHNFRCQVQFYGLSENEDWTQDRAKPVTOI 255	
Db	61 plelmfvysleervennvspsrfspcnpshflhltlqpedasylcassqvhpgrl 119			Db 61 qpikeqpalndsrclssrlrvatfvnpnrfcrqfyglisenedwtqdrakpvtoi 120	
Qy	115 AGGWSSYEQFGPCGRILTVLFDLKNVFPPEAVAFEPSSAEISHTOKLVLQATGFYFD 174			Qy 256 VSAFAWGRADCGETSESSQGMSATILEELIGKATLYAVLVSALVJMANVKRDLSRG 314	
Db	120 argg--ineqfqfpgrtritiedlknvfppeavafepssaeishqkatlvatgfypd 176			Db 121. vsaaewgradcgtstsyeqqvisatilyeilqlqkatlyavlsavlmavkrkdsg 179	
Qy	175 HYLSSWWNGKEYHSGVYSTDQPPLKEQPALNDSCVCLSSRLRVATFWNPNNPRHFRCQVO 234			RESULT 12	
Db	177 hylsswwngkeyhsvystdpplkeqpalndscvclssrlrvatfwnpnnprhfrcqvq 236			Y05/03 ID Y05/03 standard; Protein; 303 AA.	
Qy	235 FGYLSENEDWTQDRAKPVTOIVSABAAGRADCGFTSESYQGVLSATILEELIGKATLY 294			XX AC Y054/03;	
Db	237 fgyllsenedwtqdrakpvtoivsaaawgradcgftsesyqgvlsatileeligkatiye 295			XX DT 02-JUL-1999 (first entry)	

Human TCRbeta Protein fragment #1.
T cell receptor beta; TCRbeta; human; constant region;
immunosuppressor.
Homo sapiens.

JP11302299-A.
02-NOV-1999.
21-APR-1998; 98JP-0110607.
21-APR-1998; 98JP-0110607.
(KIRIN) KIRIN BREWERY KK.
WPI; 2000-075345/07.

T cell receptor beta chain constant region peptide - h
immunosuppressing activity

Disclosure: Page 11; 15PP; Japanese.

This invention describes a novel polypeptide comprising
part or all of the constant region of T cell receptor
(TCRbeta) and containing substantially no other region
having immunosuppressing activity. The TCRbeta require
of tissue-compatible antigen for the patient to be dosed
specificity. This sequence represents a fragment of the
protein described in the method of the invention.

Sequence 177 AA;

Region /label=variable 118..133

Qy 3 TRILCWAALCLIGADHTGAGYSQTPSNKVTPEKGDKVELRCDPISGHTALYWYROSLLGGQP 62
 Db 13 tllisvalfilgtkmeaattqspinkavtggvtlensqtanhnnnywyrgtghg1 72
 Qy 63 EFLIXQGTGAADDSELPLNDRFAVRPREGYSTLTKQRREQDSAYLRAQVARGWSSIN 122
 :
 Db 73 zlihysgagstekekdp-dgkyaspsqenfslllelatpsqtsvycasqdgqlgs-e 130
 Qy 123 EGYFGPDTRLIVLELDKVNVPPEAVFEPSEAEIHTQKATLYCIAATGFYPDHYESWW 182
 :
 Db 131 tlyfgstrivledrnrvpkvsfepkxaeinkqktatlvcargffpdhvrlswv 190
 Qy 183 NGKEVHSGVSTDPLQPLKEQQPALNDSRYCLSSRLRVSATFMONPRNHRFCOQFYGLSEND 242
 :
 Db 191 ngkevhsgvstdpgayke---snyscylsrlysatwhprhfrccqfqnglseed 246
 Qy 243 EWTQDRAKPYTQIVSAEAANGRADCFETSESYQQGYLSATTIYELIGKATUYAVLYSAV 302
 :
 Db 247 kwpegsbpkpvir-tsvarpgaeqcgits-syhggvisatilyeiliqkatilyavsvgv 304
 Qy 303 LMAMVKRKDS 312
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 Db 305 LMAMVKRKDS 314

Search completed: October 11, 2000, 06:08:36
 Job time: 30 sec

This image is from USPTO

16456 total number of hits containing chosen substrings searched:

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Post-processing: Minimum Match 0%

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Maximum Match 100%
Listing first 45 summaries

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No. is the number of results predicted by chance to have a score greater than or equal to the total score resulting from analysis of the total score distribution.

SUMMARY

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3	3	1332	80.0	310	US-08-891-097-4
4	4	895	53.8	314	543340-4
5	5	868.5	52.2	293	5189147-3
6	6	827	49.7	391	PCT-US95-15696-2
7	7	584.5	42.5	266	5173384-11
8	8	35.1	217	5	5189147-7
9	9	265	15.9	102	3
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11	11	239	14.4	234	US-08-487-550-2
12	12	237	14.2	235	US-08-737-939-12
13	13	236.5	14.2	215	US-08-487-753-8
14	14	228.5	13.7	213	US-08-630-820-6
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18	18	220.5	13.3	239	US-08-487-550-6
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21	21	219	13.2	242	1
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24	24	219	13.2	242	3
25	25	219	13.2	242	3
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27	27	216.5	13.0	218	2
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ALIGNMENTS

RESULT
US-08-897-097-1

; Sequence 1, Application US/08897097
; Patent No. 6034292
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,097
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIORITY DATA:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-03446 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-555-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TONGTUT01
; CLONE: 983910
; US-08-897-097-1

Query Match Score 1664; DB 3; Length 100.0%
Best Local Similarity Pred. No. 1e-169; Index 0;
Matches 314; Conservative 0; Missmatches 0;

Query Match 83 8%; Score 1394.5; DB 3; Length 311;
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 Matches 268; Conservative 14; Mismatches 29; Indels 3; Gaps 2;

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QY 241 NDEWTODRAKPPTQIVSAEANGRADGFTSESYQQGVLSATTILEILLGKATLYAVLYSA 300
 Db 241 NDEWTODRAKPPTQIVSAEANGRADGFTSESYQQGVLSATTILEILLGKATLYAVLYSA 300

QY 301 LVLMAMVKRKDSRG 314
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RESULT 3
 US-08-897-097-3
 ; Sequence 3, Application US/08897097
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; ATTORNEY: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLING, LUCY J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELEPHONE: 415-855-0555
 ; TELEX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3 :
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 ; LIBRARY: Genbank
 ; CLONE: 1100182
 ; US-08-897-097-3

Query Match 83 8%; Score 1394.5; DB 3; Length 311;
 Best Local Similarity 85.4%; Pred. No. 6.3e-141;
 Matches 268; Conservative 14; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGDVELRCDPISGHTALWYRQLSGQ 60
 Db 1 MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGDVELRCDPISGHTALWYRQLSGQ 60

QY 61 GPFELIYFQGTGAAADDGGLPDRFAVRPEGSVSTLKIQTREQDSSAYLRAGVAAGWSS 120
 Db 61 GPFELIYFQGTGAAADDGGLPDRFAVRPEGSVSTLKIQTREQDSSAYLRAGVAAGWSS 120

QY 121 YNEQYFGFGTTRILVLEDLKNYKPFPEVAVFPESEAELSHTOKATLYCLATGFYDPHVELSW 180
 Db 121 YNEQYFGFGTTRILVLEDLKNYKPFPEVAVFPESEAELSHTOKATLYCLATGFYDPHVELSW 180

QY 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 240
 Db 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 240

QY 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 177
 Db 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 177

QY 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 240
 Db 181 WNGKEYHSGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 240

QY 178 WNSKEVHSVGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 237
 Db 178 WNSKEVHSVGYSTDPOLKEPALNDSCRYCLSRLRVSATFWONPRNHFRCQVQFYGLSE 237

QY 241 NDEWTODRAKPPTQIVSAEANGRADGFTSESYQQGVLSATTILEILLGKATLYAVLYSA 300
 Db 238 NDEWTODRAKPPTQIVSAEANGRADGFTSESYQQGVLSATTILEILLGKATLYAVLYSA 300

QY 301 LVLMAMVKRKDSRG 314
 Db 298 LVLMAMVKRKDSRG 314

RESULT 3
 US-08-897-097-4
 ; Sequence 4, Application US/08897097
 ; Patent No. 6054292
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; ATTORNEY: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLING, LUCY J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELEPHONE: 415-855-0555
 ; TELEX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 4 :
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Genbank
 ; CLONE: 1100182
 ; US-08-897-097-3

; LIBRARY: GenBank
; CLONE: 339012
US-08-897-097-4

Query Match 80.0%; Score 1332; DB 3; Length 310;
Best Local Similarity 81.7%; Pred. No. 3e-134;
Matches 254; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

Qy 1 MGTRILCWAALCLGADHTGAGVSQTPSNKVTBKGDKDVELRCDPISGHTALWYRQLGQ 60
Db 1 MGTSILCWAALCLGADHTGAGVSQTPSNKVTBKGDKDVELRCDPISGHTALWYRQLGQ 60
Qy 61 GPEFLIYFGPTGAADDGLPNDRFFAVPEPGSYSTKLTKTQFQGDSAYLRAVGAAGWS 120
Db 61 GPEFLIYFGPTGAADDGLPNDRFFAVPEPGSYSTKLTKTQFQGDSAYLRAVGAAGWS 120
Qy 121 YNEQYFGPTGTRTLDLKVNPFPEPEAVFPEPSAEIISHTOKATLVCLATGFYPDHYELSW 180
Db 120 -QPQHFGDGTRLSLEDLNKFVDPKPEPEAVFPEPSAEIISHTOKATLVCLATGFYPDHYELSW 178
Qy 181 WNGKEVHSVGSTDPPQKPEQPLANDSRYCLSLRSRVLVSAFATVQNPRTFHRCOYQFYGLSE 240
Db 179 WNGKEVHSVGSTDPPQKPEQPLANDSRYCLSLRSRVLVSAFATVQNPRTFHRCOYQFYGLSE 238
Qy 241 NDEFTQDRAKPTQIVSAAWGRADCGETSESYQQGVLSATIYLEILLGKATLYAVLYSA 300
Db 239 NDEFTQDRAKPTQIVSAAWGRADCGETSESYQQGVLSATIYLEILLGKATLYAVLYSA 298

Qy 301 LVLMAMVKRD 311
Db 299 LVLMAMVKRD 309

RESULT 4
5434340-7
; Patent No. 5434340
; APPLICANT: KRIMPENFORT, PAULUS J.A.; BERNIS, ANTONIUS J.M.
; TITLE OF INVENTION: TRANSGENIC MICE DEPLETED IN MATURE
; T-CELLS AND METHODS FOR MAKING TRANSGENIC MICE
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/919,936
; FILING DATE: 27-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 820-218
; FILING DATE: 05-DEC-1988
; SEQ ID NO:7;
; LENGTH: 314

5434340-7
; SEQ ID NO:7;
; LENGTH: 314

Query Match 53.8%; Score 895; DB 5; Length 314:

Best Local Similarity 58.7%; Pred. No. 1.5e-87;
Matches 18; Conservative 34; Mismatches 86; Indels 8; Gaps 3;

Db 1.3 TTLSWVAFLCLKHMRATVSPRNVEAVFVATGKVYLSCNOTNNHNMCYRADGHTL 72

Db 1.3 TTLSWVAFLCLKHMRATVSPRNVEAVFVATGKVYLSCNOTNNHNMCYRADGHTL 72

Db 63 EFLIYFGPTGAAADDGLPNDRFFAVPEPGSYSTKLTKTQFQGDSAYLRAVGAAGWS 122

Db 73 RLIHSSYGGSTERGDIP-DGYKPSRPSQEDFSLILDLATPSQTSTVF--CASGNSAE 128

Db 123 EQYFGPGRPLRTLDLKVNPFPEPEAVFPEPSAEIISHTOKATLVCLATGFYPDHYELSW 182

Db 129 TLFGSGTIRLTVLEDRNTPPKVSLFEPSKAETANQKATLVCLARGEFFXHVELSW 188

Db 183 NGKEVHSVGSTDPPQKPEQPLANDSRYCLSLRSRVLVSAFATVQNPRTFHRCOYQFYGLSE 242

Db 189 NGKEVHSVGSTXPOAVKE --SNYSCLSLRSRVLVSAFATVQNPRTFHRCOYQFYGLSE 244

Db 243 EWTDQDRAKPTQIVSAAWGRADCGETSESYQQGVLSATIYLEILLGKATLYAVLYSA 302

Db 245 KPEGSSKPVTIONISAAWGRADCGETSESYQQGVLSATIYLEILLGKATLYAVLYSVGLY 304
Qy 303 LMAMVKRD 312
Db 305 LNANVKRKNS 314

RESULT 5
5189147-3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO:3;
; LENGTH: 293
5189147-3

Query Match 52.2%; Score 868; DB 5; Length 293;
Best Local Similarity 57.9%; Pred. No. 9.4e-85;
Matches 175; Conservative 34; Mismatches 82; Indels 11; Gaps 3;

Qy 11 LCLLGADHTGAGSYQTPSNKVTBKGDKDVELRCDPISGHTALWYRQSGGPFEFLYFGQ 70
Db 3 LCFLGRLQDVLDKVTQNTSRYLTKRMGENVILLCQDMSHEDMYWZRDQGIGLQLIYISYD 62

Qy 71 TGAADDGLPNDRFFAVPEPGSYSTKLTKTQFQGDSAYLRAVGAAGWSYYNEQYFPGBT 130
Db 63 VDSNSECDIPKG-YRSRKREHSSLIDSAKTNQTSVYFCAGAP----EQYFPGBT 115

Qy 131 RLTVLEIDLKNVPPEPEAVFPEPSAEIISHTOKATLVCLATGFYPDHVLSMWNGKEVHSG 190
Db 116 RLTVLEIDLKNVPPEPEAVFPEPSAEIISHTOKATLVCLARGEFFXHVELSWMWNGREVHSG 175

Qy 191 VSTDPOPLKEQFALNDQYCLSSLRLVSAFATVQNPRTFHRCQYQFYGLSENDETOQDRAK 250
Db 176 VSTDPOQYKE---SNYSCLSLRSRVLVSAFATVQNPRTFHRCQYQFYGLSENDETOQDRAK 231

Qy 251 PVTQIYSAEANGRADCGFTSESYQQGVLSATIYLEILLGKATLYAVLYSVLAMVKRK 310
Db 232 PVTQNIYSAEANGRADCGITASYYHQGVLSATIYLEILLGKATLYAVLYSVLAMVKRK 291

RESULT 6
PCT-US5-15696-2
; Sequence 2, Application PC/TU9515696
; GENERAL INFORMATION:
; APPLICANT: President and Fellows of Harvard College
; TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 99
; CITY: York Harbor
; STATE: Maine
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/15696
 FILING DATE:
 CLASSIFICATION:
 PRIORITY/AGENT INFORMATION:
 NAME: Farrell, Kevin M.
 APPLICATION NUMBER: US 08/349, 915
 FILING DATE: 06-DEC-1994
 CLASSIFICATION:
 ATORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 35, 505
 REFERENCE/DOCKET NUMBER: HU-9404 WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 207-363-0558
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT/US95/15696-2

Query Match 49.7%; Score 827; DB 4; Length 391;
 Best Local Similarity 62.9%; Pred. No. 4e-00;
 Matches 168; Conservative 17; Mismatches 30; Indels 52; Gaps 6;

Qy 15 GADHTGAGYSQTSPSNKVTKEKGKVTLRCDPISGHITALYWWRSLSLGQPFFLYFQFTGAA 74
 Db 150 GSDIDG-GTQSPLYLFREGQNYNTLSCEQNINHDAMYWWRDGPQGSLR-LIYY----- 201
 Qy 75 DDSGLPNDRFAVPEPGSVSITLKLTQRTQGDASAYLRAVGAWG----- 119
 Db 202 -SEIVND-----FQKGD-----TAGGSYSREKKESFPLTVTS 233
 Qy 120 -SYNQYFGPGRTRVLEDKLNVPEVPEVPESEAISHTOKATLVCLATGFYDPEVEL 178
 Db 234 AOKNPTAFGPGRTRVLEDKLNVPEVPEVPESEAISHTOKATLVCLATGFYDPEVEL 293
 Qy 179 SWWNGKEYHSGYSTDPOLKEPALNDSRYCLSSRLRVSAFEWQNPQRHFCQVOFYGL 238
 Db 294 SWWNGKEYHSGYSTDPQHKEPALNDSRYCLSSRLRVSAFEWQNPQRHFCQVOFYGL 353
 Qy 239 SENDEWTDQRAKPVTQIVSAEANGRAD 265
 Db 354 SENDEWTDQRAKPVTQIVSAEANGRAD 380

RESULT 7
 SEQ ID NO:11: 5175384-11
 APPLICANT: KRIMPENPORT, PAULUS J.A.; BURNS, ANTONIUS J.M.
 TITLE OF INVENTION: T-CELLS AND METHODS FOR MAKING TRANSGENIC MICE
 NUMBER OF SEQUENCES: 14
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/280, 218
 FILING DATE: 5-DEC-1988
 LENGTH: 266

Query Match 42.5%; Score 707; DB 5; Length 266;
 Best Local Similarity 50.2%; Pred. No. 1.5e-67;
 Matches 142; Conservative 32; Mismatches 80; Indels 8; Gaps 3;

Qy 3 TRILCWAALCLIGADHTGAGVSOTPSNKVTERGKDVLRCDFISGHITALYWWRSLSQQGP 62

Db 13 TTLSSWYALFULLGKHEAVTQSPPRNKAVTGGKVTLSNOTUNHNHYCYRADTGTL 72
 Qy 63 EFLIYFGQTGAADDGLPNDPFAVPEPGSVSITLKLTQRTQGDASAYLRAVGWSNN 122
 Db 73 RLIHYSVGLSIEKGDI-PDGKPSRPSQDFDSLLELATPSQTSVYF--CASGDNSAE 128
 Qy 123 EQYFGPGRTRVLEDKLNVPEVPEVPESEAISHTOKATLVCLATGFYDPEVEL 182
 Db 129 TLYFGSGTRVLEDLNTPPKVSLFEPSSKAELANKQATLVCLARGFPEXHVLSWWV 188
 Qy 183 NGKEVHSGVSTDPOPLKEPALNDSRYCLSSRLRVSAFEWQNPQRHFCQVOFYGLSEND 242
 Db 189 NGKEVHSGVSTDPOPLKEPALNDSRYCLSSRLRVSAFEWQNPQRHFCQVOFYGLSEE 244
 Db 245 KWPEGSPKPVTPQNAKE---SNYSYCLSSRLRVSAFEWQNPQRHFCQVOFYGLSEE 266

RESULT 8
 SEQ ID NO: 5189147-7
 APPLICANT: SAITO, HARUO; KRAZ, DAVID M.; ELSSEN, HERMAN N.;
 TONEWARA, SUSUMU
 TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCTYE RECEPTOR
 ANTIBODY

NUMBER OF SEQUENCES: 21
 CURRENT APPLICATION DATA:
 Application Number: US/07/271, 216
 Filing Date: 14-NOV-1988
 Prior Application Data:
 Application Number: 666, 988
 Filing Date: 31-OCT-1984
 Application Number: 620, 122
 Filing Date: 13-JUN-1984
 Seq ID No: 7;
 LENGTH: 217

5189147-7

Query Match 35.1%; Score 584.5; DB 5; Length 217;
 Best Local Similarity 51.8%; Pred. No. 1.3e-54;
 Matches 116; Conservative 31; Mismatches 66; Indels 11; Gaps 3;

Qy 23 VSQTPSNKVTKEKGKVTLRCDPISGHITALYWWRSLSLGQPFFLYFQFTGAAADDGGLPND 82
 Db 4 VTQMSRYLIKMGENVYLLECGQDMSEHEIMWWYRQDPGLQHQLIYTSYDSDNSGDIKXG 63

Qy 83 RFFAVPEPGSVSITLKLTQRTQGDASAYLRAVGWSNNQEYKNGPGRNLTVLEDLKNNF 142
 Db 64 -YRVSKRKREHFSLLSDAKTNOTSVYFCQGAP----EQYFGPGRTRVLEDLNNT 116

Qy 143 PPEVAVPESEAISHTOKATLVCLATGFYDPEVEL 202
 Db 117 PPKVSLFEPSSKAELANKQATLVCLARGFPEXHVLSWWVNGKVEHSGVSTDPOPLKECP 202

Qy 203 ALNDSRYCLSSRLRVSAFEWQNPQRHFCQVOFYGLSENDWTQ 246
 Db 175 -SNYSYCLSSRLRVSAFEWQNPQRHFCQVOFYGLSENDWKWE 216

RESULT 9
 Sequence 9, Application US/084663368
 Patent No.: 603539
 GENERAL INFORMATION:
 APPLICANT: Maddon, Paul J.
 APPLICANT: Littman, Dan R.
 APPLICANT: Chess, Leonard
 APPLICANT: Axel, Richard
 APPLICANT: Weiss, Robin
 APPLICANT: McDougal, J. S.

TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN T4 IN THE TREATMENT OF AIDS
 TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,550
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-4021
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 236 amino acids
 TOPOLOGY: linear
 TYPE: amino acid
 MOLECULE TYPE: Protein
 US-08-487-550-10

Query Match 14.5%; Score 243.5; DB 3; Length 236;
 Best Local Similarity 34.4%; Pred. No. 4.1e-18;
 Matches 77; Conservative 31; Mismatches 77; Indels 39; Gaps .
 Qy 23 VSQTPSNKVTEKGDKVDELRCDPISGHTA----LYWYRQLGQQPEFLIYFGTGAADD 76
 Db 30 VSGAPSQKVT-----ISC--TGSTNSNGGYDHLWYQQLPGTAPKLITY----DI 72
 Qy 77 SGLP---NDRFAVPRPEGSVSTLKIORTEQGDSAAYLRAVAAWSYYNEQYFGPGTIRLT 133
 Db 73 NRPSGTSIDRSGSK-SGTASLASLITGLQTEADYQCSDY--SSINAQVFGGGTIRLT 128
 Qy 134 VLEDLKVNFPPEVAFEPSSAEIISHTQAKATLVCLATGFYFDHVLSWVNGKEYHSGST 193
 Db 129 VLQGPKA-PSVTLFPSSSEL-QANKATLVLCLSDFEGAVTYVAKADSSSPVKGVET 185
 Qy 194 DPQPLKEQPALNDSYKLSSSLRVSATFWONPRHFRQVQFYG 237
 Db 186 -TTPSKQ---SNNKYAASSYSLTPEQWRSHS-YSCQVTHEG 223

RESULT 11
 US-08-487-550-2
 ; Sequence 2, Application US/08487550
 ; Patent No. 6113898
 GENERAL INFORMATION:
 APPLICANT: Anderson, Darrell R.
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF"
 TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,550
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:

NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 JJS-08-487-550-2

Query Match Score 237; DB 2; Length 235;
 Best Local Similarity 29.6%; Pred. No. 2e-17;
 Matches 71; Conservative 43; Mismatches 100; Indels 26; Gaps 11;

Query 6 ICWAALCL-LGADHTGAGVQST--PSNKVTEKGKDVELRC---DPISGHTALWYROS 57
 Db 1 MAWALLLILLTQTDGSWAQSLTQPAVSMSGPQSTISCTGTNNDVGSNLVNSYQQH 60

Query Match Score 237; DB 2; Length 234;
 Best Local Similarity 29.6%; Pred. No. 2e-17;
 Matches 71; Conservative 43; Mismatches 100; Indels 26; Gaps 11;

Query 58 LGQQPEPLIYFGTGAAADDGLPNDFRFAVRPEGSYSTLKIRTEGDSAAYLRAVGAAAG 117
 Db 61 PGKPKAMIVY--EVKRPQGSNRS -FSGSKSNTASLTSGLOAEDAYYCXSYAGS 115

Query 59 LQGQPEPLIYFGTGAAADDGLPNDFRFAVRPEGSYSTLKIRTEGDSAAYLRAVGAAAG 117
 Db 61 PGKPKAMIVY--EVKRPQGSNRS -FSGSKSNTASLTSGLOAEDAYYCXSYAGS 115

Query 59 LQGQPEPLIYFGTGAAADDGLPNDFRFAVRPEGSYSTLKIRTEGDSAAYLRAVGAAAG 117
 Db 61 PGKPKAMIVY--EVKRPQGSNRS -FSGSKSNTASLTSGLOAEDAYYCXSYAGS 115

Query 118 WSSYNEQYFGPOTRLVLEDLNVEPPEAVFSEAEISHTQKATLVCLATGFYDFDHVE 177
 Db 116 YT---VVFGGTKLTVLGQPKAA- PSVTLFPSSSEL-QANKATLVCLISDFYGAATV 168

Query 178 LSWWNGKEYHSVGSTDPQPPLKEQPALNDSRCLYSSLRVSATENQPRHFCQYQFYG 237
 Db 169 VAWKADSSPVKAGVET-TTPSKQ---SNKTAASSYSLTPEQWKSHRS-YSCQVTHEG 222

RESULT 1³
 US-08-480-753-8

Sequence 8, Application US/08480753
 ; Patent No. 5830675

; GENERAL INFORMATION:
 ; APPLICANT: Targan M.D., Stephan R.
 ; APPLICANT: Vidrich Ph.D., Alda M.
 ; APPLICANT: Stephan R.
 ; TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
 ; TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR
 ; TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wendy A. Whiteford, Esq.
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; APPLICATION NUMBER: US/08/480,753
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Whiteford, Wendy A.
 ; REGISTRATION NUMBER: 36,964
 ; REFERENCE/DOCKET NUMBER: P07 33571
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 622-7700
 ; TELEFAX: (213) 489-4210
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 215 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 JJS-08-480-753-8

Query Match 14.2%; Score 236.5; DB 2; Length 215;

Best Local Similarity 31.6%; Pred. No. 2e-17; Matches 81; Conservative 36; Mismatches 88; Indels 51; Gaps 15;

Qy 21 AGVQQTPSKVKVTEKGDKDYLRCDPISGHT-AIYWIYR0SLGCGSPEFLIYFQGTGAADDSG 78
Db 1 AELTQSPTLSSLSPGERATLSCRASOGSYSSAFLWYQOKAGQAAPRLIYGASRRA ---TG 57

Qy 79 LPNDRFFAVERPREGVSTLKQRTQEGDSAAYLRAGVAANGWSSYNEQY -----FGPGTR 131
Db 58 IP-DRTG-SGSQDTFTLTTRLEPEDAVY ----- YCQQYQGSSQOFTFCGPGTK 104

Qy 132 LTVLEDLK-NVFPEPEVAFEPSEAEI8HTQKATLVCLATGFYPDFHVELSWWYNGKEVHSG 190
Db 105 V---DLKRTVAAPSVEIIPPSDQLK-SGTASVCLNNFVPREAKVQWKVD-NALQSG 158

Qy 191 VSTDPOQPLKEQOPALNDSRYCLSSRLRYSATFWONPRNHFRCQYQFYGLSENDEWTQDRAK 250
Db 159 NS---QESVTEQDS-KDSTYSLSSSTLTLISKADYEK-HKRYACEVTHQGLS-----S 204

Qy 251 PVTQIVSAFAARGRADC 266
Db 205 PVT-----KSFNRESEC 215

RESULT 14
US-08-630-820-6
Sequence 6; Application US/08630820
Patent No. 6008033

GENERAL INFORMATION:
APPLICANT: OPPER, Martin
APPLICANT: BOSSLER, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CRYPTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007-5109
COUNTRY: USA
ZIP: 60666

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,603
REFERENCE/DOCKET NUMBER: 1874B/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 13.7%; Score 228,5; DB 3; Length 213;
Best Local Similarity 29.9%; Pred. No. 1.4e-16;

Matches 73; Conservative 42; Mismatches 94; Indels 35; Gaps 12;

Qy 23 VSQTPSNKVTEKGDKDYLRCDPISGHTALWYRQSLGCGSPEFLIYFQGTGAADDGGLPND 82
Db 5 MTQSPSSLSAVGDRYITCSTSSSYSMHWYQKPGKAKLITSTSNIA---SGVPSR 61

Qy 83 REFAVREPGSVSTLKIORTQEGDSAAYLRAGVAANGWSSYNEQYQFGPGRTRVLEDLKNVF 142
Db 62 -FSGSGSGTDFFTTSILOPEDATY---YCHQNSY - PTFQGQTK --VEIKRTVA 110

Qy 143 PPEVAVEPPESEAEI8HTQKATLVCLATGFYPDFHVELSWWYNGKEVHSG 190
Db 111 APSVFIFFPSDQLK-SGTASVCLNNFVPREAKVQWKVD-NALQSGNS-QESVTEQD 166

Qy 203 ALNDSRYCLSSRLRYSATFWONPRNHFRCQYQFYGLSENDEWTQDRAKPVTCQIVSAEANG 262
Db 167 S-KDSTYSLSSSTLTLISKADYEK-HKRYACEVTHQGLS-----SPVT-----KSFN 209

Qy 263 RADC 266
Db 210 RGEc 213

RESULT 15
US-07-916-098A-56
Sequence 56; Application US/07916098A
Patent No. 5871732

GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: ROSSA, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60666

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
SOFTWARE: WORD PERFECT 5.1
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
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TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: protein

US-07-916-098A-56

	Query Match	Score	DB 2;	Length
	Best Local Similarity	13.5%	224;	241;
	Matches	29.8%	Pred. No.	5.2e-16;
Qy	VSQTPSNKVTTEKGDKDVELRCDPISGHFTALY-		-WYROSILGGPPEFLIYFQGTGA	73
Db	MTQSPDSLAVSLGERATINCK-SSGSILYSFNQKNYLAWYQKPGQPKLILYWAST--		:- : : : : : : : : : : : :	81
Qy	ADDGLPNDRFRAVRPEGSVSTLKIQRTEQGDSAAVLAGVAGWSSYNEQW----		-FGP	128
Db	-RESGVP-DR-FSSGSSTDFTLTISQAEDEVAY-----		-YCQQYSSYRTFGR	127
Qy	GTRLTVLEDLKNYPPEVAVEPESEAELSHTOKATLVCLATGYPDHVELSWNGREHV		:- : : : : : : : : : : : :	188
Db	GTK---LEIKRTAAAPSVFIFPSDEQLK-SGTASVCLNNFYPREAKVQKVVD-NALQ		:- : : : : : : : : : : : :	182
Qy	SGVSTDPOPLKEPALANDSRYCCLSSRLRVSATFWQNPRNHFRCQVOFYGLSENDENTQDR		:- : : : : : : : : : : : :	248
Db	SIGNS-QESVTEQDS-KDSTYLSSTLTSKADYEK-HKVIACEVHQGLS-----		:- : : : : : : : : : : : :	229
Qy	AKPVTOIVSAEAANGRADC	266		
Db	-SPVT-----KSFRNREC	241		

Search completed: October 11, 2000, 06:09:50
 Job time: 99 sec